

SEO ID NO		
5	S14	1 TACCAAGTGCGCAACTCCACGGGGCTTTACCATGTLACCAATGATTGCCCTAACTCGAGTA
1	DK7	1 TACCAAGTGCGCAACTCCACGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
3	US11	1 TACCAAGTACGCAACTCCACGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAGTA
. 4	DR4	1 CACCAAGTGCGCAACTCTACAGGGCTTTACCATGTCACCAATGATTGCCCTAATTCGAGTA
3	DR1	1 CACCAAGTGCGCAACTCTACAGGGCTTTACCATGTCACCAATGATTGCCCTAATTCGAGTA
2	DK9	1 TACCAAGTACGCAACTCCtCGGGCCTCTACCATGTCACCAATGATTGCCCTAACTCGAGTA
6	S18	1 TACCAAGTACGCAACTCCACGGGCCTTTACCATGTCACCAATGACTGCCCTAACTCGAGCA
7	SW1	1 TACCAAGTACGCAACTCCtCGGGCCTTTACCATGTCACCAATGAtTGCCCTAACTCGAGtA
1-8	consensus	tACCAAGT-CGCAACTCcaCgGGgCTtTACCATGTcACCAATGAtTGCCCTAAcTCGAGtA
SEO ID NO:	<u>Isolate</u>	
5	S14	62 TtGTGTACGAGaCaGCtGATGCtATCCTaCACgCTCCGGGaTGTGTCCCTTGCGTTCGtGA
1	DK7	62 Tegtgtacgaggcggccgatgccatcctgcacactccggggtgtgtcccttgcgtacga
8	US11	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCGGGGTGTGTtCCTTGCGTTCGCGA
4	DR4	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACACGCCGGGGTGTGTCCCTTGCGTTCGCGA
3	DR1	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCACGCGCGGGGTGTGTCCCTTGCGTTCGCGA
2	DK9	62 TTGTGTACGAGGCGGCCGATGCCATCCTGCALTCTCCAGGGTGTGTCCCTTGCGTTCGCGA
6	S18	62 TTGTGTACGAGACGGCCGATaCCATCCTACACTCTCCGGGGTGTGTCCCTTGCGTTCGCGA
7	SW1	62 TTGTGTACGAGACGGCCGATGCCATtCTACACTCTCCAGGGTGTGCCCTTGCGTTCGCGA
1-8	consensus	TtGTGTACGAGgCgGCcGATgCcATcCTgCAc-CtCCgGGgTGTGTcCCTTGCGTTCGcGA
SEO ID NO:	<u>Isolate</u>	
5	S14	123 GGGTAACACCTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCCACCAGGGACGGCAAA
1	DK7	123 GGGTAACGtCTCGAGGTGTTGGGTGGCGATGACCCCCACGTGGCCACCAGGGGA+CGGAAA
8	US11	123 GGGTAACGCtTCGAGGTGTTGGGTGGCGATGACCCCCACGGTGGCGACGCGACGGACG
4	DR4	123 GGGTAACaCCTCGAGGTGTGGGTGGCCGCCACCAGGGACGGCAAA
3	DR1	123 GGGTAACGCCTCGAGGTGTTGGGTGGCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAA
2	DK9	123 GGGTAACGCCTCGAaATGTTGGGTGGCGGTGGCCCCCACGGTGGCCACCAGGGACGGCAAg
6	S18	123 GGGTAACGCCTCGAGATGTTGGGTGCCGGTGGCCCCCACAGTTGCCACCAGGGACGGCAAA
7	SW1	23 GGaTggCGCCcCGAagTGTTGGGTGgCGGTGGCCCCCACAGTcGCCACLAGGGACGGCAAA
1-8	consensus	GGgTaaCgcctCGAggTGTTGGGTGgCGgTGaCCCCCACgGTgGCCACcAGGGAcGGCAAa

CEO ID NO.	Taalaha		·
SEO ID NO:	<u>Isolate</u> S14	184	CTCCCCGCAaCGCAGCTTCGACGTLACATCGATCTGCTLGTCGGGAGcGCCACCCTCTGTT
_			
1	DK7	184	CTCCCACAGCGCAGCTTCGACGTCACATCGATCTGCTCGGGGAGtGCCACCCTCTGTT
8	· US11	184	CTCCCCACACGCACTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGTT
4	DR4	184	CTCCCCACAACGCAGCTCCGACGTCACATCGACCTGCTTGTCGGGAGCGCCACCCTCTGCT
3	DR1	184	CTCCCCACACGCAGCTTCGACGTCACATCGACCTGCTTGTCGGGAGCGCCACCCTCTGCT
2	DK9	184	CTCCCCGCAACGCAGCTTCGACGTCACATCGATCTGCTTGTCGGGAGCGCCACCCTCTGCT
6	S18		
7			
	SW1	184	CTCCCtGCAACGCAGCTTCGACGTCACATCGATCTGCTTGT-GGAAGCGCCACCCTCTGCT
1-8	consensus		CTCCCc-CAaCGCAgCTtCGACGTcACATCGAtCTGCTtGTcGGgAGcGCCACCCTCTGcT
SEO ID NO:	<u>Isolate</u>		
5	\$14	245	CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTTCTTGTCGGTCAgCTGTTTACCTT
1	DK7		CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTGTCGGTCAACTGTTTACCTT
8	S11	245	CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTT
4	DR4		
_			CGGCCTCTACGTGGGGGACTGTGCGGGTCTGTCTTGTCGGTCAACTGTTCACCTT
3	DR1	245	CGGCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTGTCGGTCAACTGTTCACCTT
2	DK9	245	CGGCCCTCTATGTGGGGGAC+TGTGCGGGTCTGTCTTCCTTGTCGGCCAACTGTTCACCTT
6	S18	245	CGGCCCTCTATGTGGGGGACCTGTGCGGGTCTGTCTTTCTT
7	SW1	245	CGGCCCTCTAcGTGGGGGACtTGTGCGGGTCTGTCTTTCTcGTCAGtCAaCTGTTCACgtT
1-8	consensus		CGGCCCTCTAcGTGGGGGAC-TGTGCGGGTCTGTCTTtCTtGTCgGtCAaCTGTTcACctT
SEO ID NO:	<u> Isolate</u>		
5	S14	306	CTCTCCCAGGCGCCtCTGGACGACGCCAAGaCTGCAATTGTTCTATCTATCCcGGCCATATA
1	DK7	306	CTCTCCCAGGCGCCACTGGACGACGCAAGGCTGCAATTGTTCTATCTA
8	S11	306	CTCTCCCAGaCGCCACTGGACGACGCAGGCCTGCAATTGTTCTATCTATC
4	DR4		
3	DR1		
2	DK9		
			CTCCCCAGaCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTACCCCGGCCATATE
6	S18		CTCCCCAGGCGCCACTGGACAACGCAAGACTGCAACTGTTCTATCTA
7	SW1	306 (CTCCCCCAGGCGCCACTGGACAACGCAAGACTGLAACTGTTCTATCTALCCCGGCCACATA
1-8	consensus	•	CTCtCCCAGgCgCCaCTGGACaACGCAAGaCTGCAAtTGTTCtATCTAtCCcGGCCAtATa

SEO ID NO:	Isolate	
5	S14	367 ACGGGTCAtCGCATGGCATGGGATATGATGATGAACTGGTCCCCTACGACGGCacTGGTAG
1	DK7	367 ACGGGTCACCGCATGGCgTGGGATATGATGATGACTGGTCCCCTACcACGGCGTTGGTAG
8	S11	367 ACGGGTCACCGCATGGCaTGGGATATGATGATGAACTGGTCCCCTACGgCGGCGTTGGTgG
4 .	DR4	367 ACGGGCCACCGCATGGCGTGGGATATGATGATGATGATCCCCTACGACAGCGCTGGTAG
3	DR1	367 ACGGGACACCGLATGGCATGGGATATGATGATGAACTGGTCCCCTACGACAGCGCTGGTAA
2	DK9	367 ACGGGTCAtCGCATGGCGTGGGATATGATGATGAACTGGTCCCCTACAGCAGCGCTGGTAA
6	S18	367 ACGGGTCACCGLATGGCATGGGATATGATGAACTGGTCCCCTACAACGGCGLTGGTAA
7	SW1	367 ACGGGTCACCGCATGGCATGGGATATGATGAACTGGTCCCCCACAACaGCGCTGGTAG
1-8	consensus	ACGGGtCAcCGcATGGCaTGGGATATGATGAACTGGTCCCCtACgaC-GCgcTGGTag
SEO ID NO:	Isolate	
5	S14	428 TAGCTCAGCTGCTCCGGATCCCaCAAGCCATCTTGGALATGATCGCTGGTGCTCACTGGGG
1	DK7	428 TAGCTCAGCTGCTCCGGATCCCGCAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
8	S11	428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGCTCACTGGGG
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGTGCCCACTGGGG
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCACAAGCCATCTTGGACATGATCGCTGGAGCCCACTGGGG
2	DK9	428 TGGCgCAGCTGCTCAGGATCCCGCAgGCCATCTTGGACATGATCGCTGGTGCCCACTGGGG
6	S18	428 TAGCTCAGCTGCTCAGGGTCCCGCAAGCCGTCTTGGACATGATCGCTGGTGCCCACTGGGG
7	SW1	428 TAGCTCAGCTGCTCAGGATCCCGCAAGCCGTCTTGGACATGATCGCTGGTGCCCACTGGGG
1 - 8	consensus	TagCtCAgCTGCTCcGGaTCCC-CAaGCCaTCTTGGAcATGATCGCTGGtGCcCACTGGGG
SEO ID NO:	<u>Isolate</u>	
5	S14	489 AGTCCTAGCGGCATAGCGTATTTCTCCATGGTGGGAAACTGGGCGAAGGTCCTAGTgGTG
1	DK7	489 AGTCCTGGCGGGCATAGCGTATTTTTCCATGGTGGGGAACTGGGCGAAGGTCCTGGTAGTG
8	S11	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCCTGGTAGTG
4	DR4	489 AGTCCTAGCGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCCTGGTAGTG
3	DR1	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCGTGGTAGTG
2	DK9	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGTGGGGAACTGGGCGAAGGTCGTGGTgGTa
6	S18	489 AGTCTAGCGGGCATAGCGTATTTCTCCATGGCGGGAACTGGGCGAAGGTCCTGCTAGTG
7	SW1	489 AGTCCTAGCGGGCATAGCGTATTTCTCCATGGtGGGGAACTGGGCGAAGGTCCTGATAGTG
1-8	consensus	AGTCCTaGCGGGCATAGCGTATTTcTCCATGGtGGGGAACTGGGCGAAGGTCcTggTaGTg

SEO ID NO	<u>: Isolate</u>		
· 5	S14	550	CTGCTGCTATTCGCCGGCGTtGACGCG
_	5.00		
1	DK7	550	CTGCTGCTATTTGCCGGCGTCGACGCG
8	US11	550	
•	0511	550	CTGCTGCTATTTGCCGGCGTCGACGCG
4	DR4	550	
*	DR4	550	CTGTTGCTGTTTGCCGGCGTTGATGCG
3	DR1	550	
3	DRI	350	CTGTTGCTGTTTGCCGGCGTTGATGCG
2	DK9	550	CTGTTGCTGTTTaCCGGCGTCGATGCG
-	5.0	330	
6	S18	550	CTGTTGCTGTTTgCCGGCGTCGATGCG
•	510	330	
7	SW1	550	CTGTTGCTGTTTtCCGGCGTCGATGCG
•	5111	230	CIGITACIGITICCCGGCGTCGATGCG
1-8	consensus		CTGtTGCTgTTtqCCGGCGTcGAtGCG

SEO ID	NO: Isolate		
11	DK1	1	TATGAAGTGCGCAACGTGTCCGGGGTGTACCACGTCACAACGACTGCTCCAACTCAAGCA
24	T10	1	TATGAAGTGCGCAACGTGTCCGGGATGTACCAtGTCACGAACGACTGCTCCAACTCAAGCA
10	. дз	-	TATGAAGTGCGCAACGTGTCCGGGGTGTACCAGGTCACCAAACACTCTTCCAACTACCAACAA
10	D3		TATGAAGTGCGCAACGTGTCCGGGGTGTACCAAGTCACAAtGACTGTTCCAACTCGAGCA
9	D1	1	TATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGA
14	HK5	1	TATGAAGTGCGCAACGTGTCCGGGGTATACCATGTCACGAACGA
15	*****	_	
15	HK8	1	TATGAAGTGCGCAACGTGTCCGGGATATACCATGTCACGAACGA
12	нк3	1	TATGAAGTGCGCAACGTGTCCGGGATATACCATGTCACGAACGA
		•	TATGAAGTGCGCAACGTGTCCGGGATATACCATGTCACGAACGA
23	T 3	1	TACGAAGTGCGCAACGTGTCCGGGGTGTACLATGTCACGAACGACTGTTCCAACTCAAGCA
22	SW2	1	TATGAAGTGCGCAACGTGTCCGGGGTGTALCATGTCACGAACGACTGTTCCAACTCAAGCA
17	IND8	•	TATCA - CTCCCCCA A COTTOTTO CONTROL CO
1,	11100	_	TATGAGGTGCCCAACTCAAGTA
16	IND5	1	TATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGA
21	SA10	1	TATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGA
20	045	_	
20	S45	1	TATGAAGTGCGCAACGTGTCCGGGGCTACCATGTCACGAACGA
25	US6	1	TATGAAGTGCGCAACGTGTCCGGGATGTACCATGTCACGAACGA
		-	
13	HK4	1	CATGAAGTGCaCAACGTaTCCGGGATCTACCATGTCACGAACGACTGCTCCAACTCAAGTA
18	P10	1	TATGAAGTGCGCAACGTGTCCGGGGTGTACCATGTCACGAACGA
19	S9	٦.	TATE A CICCOCA A COTT - TOOCCOCA - CTT - C
* -	33	1	TATGAAGTGCGCAACGTaTCCGGGGCGTACCATGTCACGAACGACTGCTCCAACTCAAGTA
9-25	consensus		tAtGAaGTGCgCAACGTgTCCGGGgtgTAccAtGTCACqAAcGACTGcTCCAACTcaAGca

SEO ID NO:	<u> Isolate</u>		
11	DK1	62 TCGTGTATGAGGCAGtGGACGTGATCATGCAtACCCCaGGGTGCGTGCCCTGCGTTCC	3GGA
24	T 10	62 TEGTGTETGAGGCAGCGGACETGATCATGCACACCCCGGGTGCGTCCGGTGCGGTG	
27	140	62 TEGIGIETGAGGCAGCGGACETGATCATGCACACCCCCGGGTGCGTGCCCTGCGTTCG	3GGA
10	D3	62 TCGTGTATGAGACAGCGGACATGATCATGCACACCCCCGGGTGCGTGC	GGA
•	-		
9	D1	62 TEGTGTATGAGACAGCGGACATGATCATGCACACCCCGGGTGCGTGC	GGA
14	HK5	62 TCGTGTACGAGACAACGGACATGATCATGCACACCCCTGGGTGCCTTCCCCTTCCCCTTCCCCTTCCCCTTCCCCTTCCCCTTCCCC	
			III
15	HK8	62 TCGTGTATGAAACAGCGGACATGATLATGCATACCCCTGGATGCaTGCCCTGCGTTCG	GGA
12	нк3	62 TCGTGTATGAGACAGCAGACATGATCATGCATACCCTCGATGCGTGCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTTCTTCTTCTTCTTCTTCTTCTTTCTTCTTCTTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTC	111
	•	1	iGGA
23	T3	62 TTGTGTATGAGACAGCGGACATGATCATGCACACCCCTGGGTGCGTGC	GGA
22	SW2	62 TTGTGTATGAGACAGCGGACATGATCATGCA+ACCCCGGGTCCGTCCGGTCCG	111
	3#2	** ITGIGIAIGAGACAGCGGACATGATCATGCAEACCCCCGGGTGCGTGCCCTTGCGTTCG	GGA
17	IND8	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGC	GGA
16	IND5		111
16	INDS	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACtCCCGGGTGCGTGCCTTCG	GGA
21	SA10	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCCGGGTGCGTGC	 GGA
20	0.45		III
20	S45	62 TTGTGTATGAGGCAGLGGACGTGATCCTGCACACCCCLGGGTGCGTGCCTGCGTTCG	GGA
25	US6	62 TTGTGTATGAGGCAGCGGACATGATCATGCACACCCCGGGTGCGTGC	
			LII
13	HK4	62 TTGTGTATGAGGCAGCGGACATGATCATGCALACCCCCGGGTGCGTGCCCTGcGTcCG	GGA
18	P10	62 TTGTGTATGAGGCAGCGGACATGATAATGCCACACCCCGGGTCCCTCCC	
			GGA III
19	S9	62 TTGTGTACGAGGCAGCGGACGTGATCATGCALACCCCCGGGTGLGTaCCCTGCGTTCa	GGA
9 - 25	consensus	TtGTGTatGAggCAgcgGACaTGATcaTGCAcACcCCcGGqTGcqTqCCCTGcGTtCq	

SEO ID NO	<u> Isolate</u>		
11	DK1	123	GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCACcCCCACGCTCGCGGCCAGGAACgCCAGC
24			
24	T10	123	GGGCAACTCCTCCCGCTGCTGGGTAGCGCTCACtCCCACGCTCGCGGCCAGGAACACCAGC
10	D3	123	GGACAACTCCTCTCGCTGCTGGGTAGCGCTCACCCCCACGCTCGCGGGCTAGCAATACCAACTA
9	D1	123	GGACAACTCCTCTCGCTGGGTAGCGCTCACCCCCACGCTCGCGGCTAGGAATGGCAaC
	1		
14	HK5	123	AAACAACTCCTCCCGTTGETGGGTAGCGCTCGCCCCACGCTCGCGGCCAGGAACGCCAGC
15	HK8	123	GAACACTCCTCCCGTTGcTGGGTgGCGCTCACTCCCACGCTCGCGGCtAGGAAtGTCAGC
			GAACAACICCTCCCGTIGCTGGGTGGCGCTCACTCCCACGCTCGCGGCtAGGAAtGTCAGC
12	нк3	123	GAACAACTCCTCCCGCTGtTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGTCAGC
22			- 1
23	Т3	123	GAGCAALTCCTCCCGCTGCTGGGTAGCGCTLACTCCCACGCTCGCGGCCAGGAACGCCAGC
22	SW2	122	GGCAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTTTTTTTT
	5,12	123	GGCCAACICCICCGCTGCTGGGTAGCGCTCACTCCCACGCTAGCAGCCAGGAACACCAGC
17	IND8	123	GGGCAACTECTCTaGETGCTGGGTAGCGCTCACTCCCACTCTCGCGGCLAGGAACGCCAGC
16	IND5	123	GGGCAACTCCTCTCGCTGCTGGGTAGCGCTCACTCCCACTCTCGCGGCCAGGAACGCCAGC
21	SA10	122	GAACAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTTCGCCCCCACGAAAAAAAA
	OFILO	123	GAACAACTCCTCCCGCTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACTCCAGC
20	S45	123	GAACAACTCCTCCCGtTGCTGGGTgGCGCTCACTCCCACGCTCGCGGCCAGGAACTCCAGC
25	US6	123	GAACAAtTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACGCTCGCGGCCAGGAACGCtAGC
13	HK4	122	GAACAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCCACGCTCGCGCCAACCAACC
	111/3	123	HILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
18	P10	123	GAACAACTCCTCCCGcTGCTGGGTAGCGCTCACTCCCACACTCGCGGCLAGGAALLCCAGC
19	S9	123	GggtAACTCCTCCCaaTGCTGGGTgGCGCTCACcCCCACgCTCGCGGCCAGGAAcgCtAcC
9 - 25	consensus		gaacAActcCTCccgcTGcTGGGTaGCGCTcaCtCCCACgCTcGCgGCcAGGAlcgcclgC

SEO ID NO	: <u>Isolate</u>		
11	DK1	184	aTCCCCACTACGACAATACGACGCCATGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
24	T10	184	GTCCCCACTACGACGATACGACGCCATGTCGATTTGCTCGTTGGGGGCGGCTGCTTTCTGCT
10	. D3	184	GTCCCCACTACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGGCGCTTGCTT
9	D1	184	GTCCCCACTACGGCGATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
14	HK5	184	GTCCCCACCACGCAATACGACGCCACGTCGACTTGCTCGTTGGGGCGGCTGCTTTTCTTCTT
15	HK8	184	GTCCCCACLACGACAATACGACGCCACGTCGACTTGCTCGTTGGGGGCGCCGCTTCCTTTTCTTCTT
12	HK3	184	GTCCCCACACGACAATACGACGTCACGTCGACTTGCTCGTTGGGGGGGG
23	T3	184	GTCCCCACTAaGACAATACGACGTCACGTCGACTTGCTCGTTGGGGGCGGCTGCTTTCTGtT
22	SW2	184	GTCCCCACTACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGcT
17	IND8	184	GTCCCACACACACACACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
1.6			
16	IND5	184	GTCtCCACCACGACAATACGACaCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGTT
21	224		
21	SA10	184	GTCCCCACTACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
20	045		
20	S45	184	GTCCCCACTACGACAATACGACGECACGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
25	US6		
. 23	056	184	GTCCCCACTACGACAATACGACGCCACGTCGATTTGCTCGTTGGGGCGGCTaCTTTCTGCT
13	HK4	304	
. **	nr4	184	aTCCCCACTACGACAATACGACGCCATGTCGACTTGCTCGTTGGGGCGGCTGCTTTCTGCT
18	P10	7.04	
	PIU	184	GTCCCaACTACGGCAATACGACGCCATGTCGATTTGCTCGTTGGGGCGGCTGCTTTCTGCT
19	S9	104	
	33	184	GTCCCcACcACGaCAATACGACGtCATGTCGATTTGCTCGTTGGGGCGGCTGtTTTCTGCT
9-25	consensus		
-	C0.15C116U6	'	gTCcCcACtAcGaCaATACGACgcCAcGTCGAtTTGCTCGTTGGGGCGGCTgctTTCTGcT
			-

SEO ID NO	: <u>Isolate</u>		
11	DK1	245	CCGCTATGTACGTGGGGGACCTCTGCGGATCcGTTTTCCTCGTCTCTCAGCTGTTCACCTT
20.			
24	T10	245	CCGCTATGTAtGTGGGGAGACCTCTGCGGATCTGTTTTCCTCGTCTCTCAGCTGTTCACCTT
10	D3	245	CCGCCATGTACGTGGGGGATCTTTGCGGGATCTGTTTCCTCGTCTCCCAGCTGTTCACCTT
9	. D1	245	
9		245	CCGCCATGTACGTGGGGGATCTGTGTTTTCCTCATCTCCCAGCTGTTCACCCT
14	HK5	245	CCGCTATGTACGTGGGGGATCTtTGCGGATCTGTTTTCCTCTTTCCGATCTTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCA
	CAN	243	CCGCIAIGIACGTGGGGGATCTETGCGGGATCTGTTTTCCTCCTCTCCCAGCTGTTCACCTT
15	нк8	245	CCGCTATGTACGTGGGGGATCTCTGCCGATCTCTTTTTTCCTCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCTCCCACCTCCACCA
75		243	COSTANTANTANTANTANTANTANTANTANTANTANTANTANT
12	нкз	245	CCGCTATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCT+GTCTCCCACCTGTTTCA
	_		
23	T3	245	CCGCTATGTACGTGGGGGATCTCTGCGGATCTCTTCTCT
			III IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
22	SW2	245	CCGETATGTACGTGGGGGATCTCTGCGGATCTGTTTTCCTCGTCTCCCAGCTGTTCACTGTT
/			
17	IND8	245	CCGCTATGTACGTGGGGGATCTCTGCGGGTTTTTCCTLGTCTCCCAGCTGTTCACCTT
3.6			
16	IND5	245	CCGCTATGTACGTGGGGGATCTaTGCGGATCTGTTTTCCTcGTCTCCCAGCTGTTCACCTT
21	SA10	245	
21	SAIU	245	CCGCcATGTACGTGGGGGACCTCTGCGGATCTGTTTTCCTTGTCTCCCAGCTGTTCACCTT
20	S45	245	CCGCTATGTACGTGGGGGAtCTCTGCGGATCTGTTTTTCCTTGT+TCCCAACGTCTTGTA
	343	243	CCCCIAIGIACGIGGGGAECICTGGGGATCTGTTTTCCTTGTETCCCAGCTGTTCACCTT
25	US6	245	CCGCTATGTACGTGGGGGACCTCTGCGGGTTTTTCCTCaTCTCCCACCTGTTCACCTTTT
			CCGCTATGTACGTGGGGGACCTCTGCGGGTCCGTTTTCCTCaTCTCCCAGCTGTTCACCTT
13	HK4	245	CCGCcATGTACGTGGGaGATCTCTGCGGGATCTGTCTCCTCCTCCCAG+TGTTCCACCTTCTCCAG+TGTTCCACCTTCTCCAG+TGTTCCACCTTCCAG+TGTTCCACCTTCCAG+TGTTCCACCTTCCAG+TGTTCCACCTTCCAG+TGTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACCTTCACA
		_	
18	P10	245	CCGCTATGTACGTGGGGGATCTCTGCGGGATCTGTTCTCCTCGTCTCCAGCTGTTTCACCTTTT
19	S9	245	CCGCTATGTACGTGGGGGAcCTgTGCGGATCTGTTtTCCTCaTCTCCCAGCTGTTCACCaT
0.05			
9-25	consensus		CCGctATGTAcGTGGGGGAtCTcTGCGGaTCtGTttTCCTcqTcTCcCAGcTGTTCACctT

SEO ID NO	: <u>Isolate</u>		
11	DK1	306	tTCaCCTCGCCGGCATGAGACagcaCAGGACTGCAACTGCTCAATCTATCCCGGCCAcgTt
24	m 10		
24	T10	306	CTCGCCTCGCCGGCATGAGACttTgCAGGACTGCAACTGCTCAATCTATCCCGGCCAtcTG
10	D3	306	CTCGCCTCGCCGGCATGAGACACTACAGGAATGTAACTGCTCAATGTATAGGGGGGAAGGAA
		300	CTCGCCTCGCCGGCATGAGACAGTACAGGAATGTAACTGCTCAATCTATCCCGGCCACGTG
9	D1	306	CTCGCCTCGCCGGCATGAGACGGTACAGGAGTGTAALTGCTCAATCTATCCCGGCCACGTG
14	HK5	306	CTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
15	нк8	200	
**	nko	306	tTCGCCTCGCCGACACGAGACGGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
12	нкз	306	CTCGCCTCGCCGACACGAGACACTACAGGACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACTCAACT
23	T 3	306	CTCGCCTCGCCGGCAtGAGACAGTACAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
22			
22	SW2	306	tTCACCTCGCCGGCAcGAGACAGTACAGGACTGCAACTGtTCCATCTATCCCGGCCACGTA
17	IND8	306	CTCACCGCGCCGGCATGAGACAGTACAGGACTGCCATTCTATTCCCCCGCGCATGCTACTATTCCCCCCGCCATGCTACTATTCCCCCCCC
	25.25	300	
16	INDS	306	CTCACCGCGCCGCATGAGACAGTACAGGACTGCAATTGCTCCATCTATCCCGCCCACGTA
21	SA10	306	CTCGCCTCGCCGGtATGAGACAGTACAGGACTGCAATTGCTCAATCTATCCCGGCCGCGTA
20	S45	30 <i>6</i>	CTCCCCTCCTCCCCCTTCCCCCTTCCCCCTTCCCCCTTCCCC
	043	300	CTCGCCTCGTCGGCATGAGACAGTACAGGACTGCAACTGTTCAATCTATCCCGGCCACGTA
25	US6	306	CTCGCCTCGTCaGCATGAGACAGTACAGGACTGCAATTGTTCAATCTATCCCGGCCACGTA
13	HK4	306	CTCGCCTCGCCGGCATGAGACGGTACAGGACTGCAATTGCTCAATCTATCCCGGCCACGTA
18	P10		111
*0	PIU	306	CTCaCCTCGCCGGCATtgGACAGTACAGGACTGCAATTGtTCAATCTATCCtGGCCACGTA
19	S9	306	CTCgCCcCGt CGGCATgaGACACTACACA a CTCCCA A CTCCA A CTCCCA A CTCCCA A CTCCA A CTCCCA A CTCCCA A CTCCCA A CTCCA A
			CTCgCCcCGtCGGCATgaGACAGTACAGAACTGCAATTGcTCAATCTATCCcGGaCACGTg
9 - 25	consensus	1	cTCgCCtCGcCggcAtgaGACagtaCAGqAcTGcAAcTGcTCaaTCTATCCcGgcCaccTa

SEO ID N	O: <u>Isolate</u>		
11	DK1	367	TCAGGTCACCGCATGGCTTGGGALATGATGATGAACTGGTCACCTACAACAGCcCTAGTGC
•			
24	T10	367	TCAGGTCACCGCATGGCTTGGGACATGATGATGAACTGGTCGCCTACAACAGCtCTAGTGG
10			
10	· D3	367	ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCTACAGCAGCCCTAGTGG
9	D1	267	
,	DI	36/	ACAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCtTAGTGG
14	HK5	367	ACAGGT CACCGCATGGCTTGGGATATGATGATGATGATGATGATGATGATGATGATG
	111.5	367	ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCCTAGTGG
15	HK8	367	TCAGGTCACCGCATGGCTTGGGATATGATGATGATGGTCGCCCACACACA
		30,	1CAGGTCACCGCATGGCTTGGGGATATGATGATGATCTGGTCGCCCACAACAGCCCTAGTGG
12	нкз	367 '	TCAGGTCACCGCATGGCTTGGGATATGATGATGATGATCCCCC+ACA-CACCCCTACTACTACTACTCCCCTACTACTACTACTACTCCCCTACTA
			TCAGG TCACCGCATGGCTTGGGATATGATGATGACTGGTCCCCCACAGCAGCCCTAGTGG
23	T 3	367	aCAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCGCCCACACACGCCCTAGTCG
			aCAGGTCACCGEATGGCTTGGGATATGATGATGACTGGTCGCCACAACGGCACTAGTGG
22	SW2	367 3	TCAGGTCACCGCATGGCTTGGGACATGATGATGAACTGGTCACCTACAGCAGCCCTgGTGG
			````````````````````````````\\\\\\\\\\
17	IND8	367 3	TCAGGTCACCGCATGGCTTGGGATATGATGATGACTGGTCACCTACAGCgGCCCTAGTGG
3.6			}
16	IND5	367 7	TCAGGTCACCGCATGGCCTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
21	SA10	267	
	SAIU	36/#	ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAaCAGCtCTAGTaG
20	S45	267 7	ACAGGTCACCGCATGGCTTGGGATATGATGATGATGATGATGATGATGATGATGATG
_,	J13	36/ }	ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCTACAGCAGCCLTAGTGG
25	US6	367 1	CCAGGTCACCGCATGGCTTGGGATATGATGATGAALTGGTCACCTACACCACCGCTACTACACCACCCCTACTACACCACCCCTACTACACCAC
		1	1
13	HK4	367 7	CAGGTCACCGCATGGCTTCGGATATGATCATCATCATCATCATCATCATCATCATCATCATCATCA
		Ī	
18	P10	367 T	CAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACAGCAGCCCTAGTGG
19	S9	367 a	ACAGGTCAtCGCATGGCcTGGGATATGATGATGAACTGGTCGCCtACAaCAGCCCTAGTGG
0.05			
9-25	consensus	t	CAGGTCAcCGcATGGCtTGGGAtATGATGATGAAcTGGTCaCCtACAgCaGCccTaGTgg
			and the second s

SEO ID NO	<u> Isolate</u>		
11	DK1	428	TaTCGCAGTTACTCCGaATCCCACAAGCTGTCgTGGACATGGTGgCgGGGCCCACTGGGG
24	<b>T10</b>		
2.3	110	428	TgTCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGaCaGGGGCCCACTGGGG
10	D3	428	TATCGCAGTTACTCCGGATCCCACAAGCTGTCgTGGACATGGTGGCGGGGGCCCACTGGGG
_			
9	D1	428	TATCGCAGTTACTCCGGATCCCACAAGCTGTCaTGGACATGGTGGCGGGGCCCACTGGGG
14	HK5	428	TGTCGCAGTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTaGCGGGGGCCCACTGGGG
15	uvo		
15	HK8	428	TGTCGCAGTTACTCCGGATCCCGCAAGCTaTCGTGGACATGGTGGCGGGGGCCCACTGGGG
12	HK3	428	TGTCGCAaTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
23	Т3	428	TGTCGCAGTTaCTCCGCATCCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACCTCACAACA
22	SW2		TATEGER ATTECCE ATTECCE AND ACCOUNT AND AC
17	IND8	428	TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGGACATGGTAGCGGGGGCCCACTGGGG
16	IND5	428	TATCGCAGTTGCTCCGGATCCCACAAGCTGTCGTGGATATGGTGGCGGGGGCCCACTGGGG
21	SA10	428	TATCGCAGTTACTCCGGATCCCACAAGCTATCGTGGACATGGTGGCGGGGGCCCACTGGGG
20	S45	428	TATCGCAGTTACTCCGGATCCCACAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
25	US6	428 '	TATCGCAGTTACTCCGGATCCCACAACCTCATCATCATCATCATCATCATCATCATC
13	HK4		
	333.2		TATCGCAGTTACTCCGacTCCCACAAGCTGTCATGGACATGGTGGCGGGGGCCCACTGGGG
18	P10	428	TGTCGCAGCTACTCCGGATCCCACAAGCTATCLTGGATGTGGTGGCGGGGGCCCACTGGGG
19	S9	428	TATCGCAGCTACTCCGGATCCCACAAGCTGTCATGGATATGGTGGCGGGGGCCCACTGGGG
9-25	consensus		PatcGCAgttaCTCCGgatCCCaCAAGCTgTCgTGGAcaTGGTggCgGGGGCCCACTGGGG

<u> Isolate</u>		
DK1	489	AGTCCTGGCGGGCCTCGCCTACTACTCCATGGCGGGGAACTGGGCCAAGGTTTTAATTGTG
<b>T10</b>	489	AGTCCTGGCGGGCCTtGCCTACTATTCCATGGCGGGAACTGGGCTAAGGTTTTAATTGTG
		AGICEIGGEGGEEIEGEEIACIATICEAIGGEGGGGAACIGGGETAAGGTTTTAATTGTG
D3	489	GGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGCTTAACGTTGATGGTGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGAACTGGGGAACTGGGGAACTGGGGAACTGGGGAACTGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGAACTGGAACTGGGGAACTGGAACTGGAACTGGGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA
		GGICCIGGCGGGCTAGGTTTTGATTGTG
D1	489	GGTCCTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAACTGGGCTAACGGTTAACGTTGGTGGGGAACTGGGCTAACGTTGATGGTGGGGAACTGGGGTAACGTTAACGTTGGTGGGGAACTGGGGTAACGGTTAACGTTGGTGGGGAACTGGGGTAACGGTTAACGTTGGTGGGGAACTGGGGTAACGGTTAACGTTGGTGGGGAACTGGGGTAACGGTTAACGTTGGTGGGGAACTGGGGGTAACGGTTAACGTTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACGAACAAC
HK5	489	GGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGAAACTGGGCTAAGGTTTTGATTCTG
		GGICCIGGCGGGCCIIGCCIACTATICCAIGGTGGGAAACTGGGCTAAGGTTTTGATTGTG
HK8	489	AGTCCTAGCGGGCCTTGCCTACTATTCCATGGTGGGCAACTGGGCTAAGGTTTTGATTGTG
		AGICCIAGCGGCCIGCCIACIATICCATGGTGGGCAACTGGGCTAAGGTTTTGATTGTG
нкз	489	AGTCCTAGCGGGCCTTGCCTACTATTCCATGGTGGGAAACTGGGCTAAGGTTTTCTG
		AGICCIAGCGGGCCIIGCCTACTATICCATGGTGGGGAACTGGGGCTAAGGTTTTGATTGTG
тз	489	AGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGGTAACGTTAACGTTTTCTATTCTTC
		AGICCIGGCGGGCCIIGCCIACTATICCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTG
SW2	489	AGTCCTGGCGGGCCTTGCaTACTATTCCATGGTGGGAACTCCCCTDAACGTGAACAACAACAACAACAACAACAACAACAACAACAACAAC
	-03	AGICCIGGCGGCCTIGCATACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTG
IND8	489	AATCCTGGCGGGCCTTGCCTACTATTCCATGGTAGGGAACTGGGGTAACGGTAACGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGAACTGGGGAACTGGAACTGGAACTGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGAACTGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTG
		ARICCIGGCGGCCIIGCCTACTATTCCATGGTAGGGAACTGGGCTAAGGTTTTGATTGTG
IND5	489	AATCCTGGCGGGCCTTGCCTACTATTCCATGGTAGGGAACTGGGCTAACGTTAACGTTAACGTTAACGGTAACGGGAACTGGGGTAACGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGGGGGAACTGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGGAACTGAACTGGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGA
		ALICCIOGCOGOCCIIGCCIACTATTCCATGGTAGGGAACTGGGCTAAGGTTTTGATTGTG
SA10	489	AGTCCTaGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTCATTCT+
		ASTECTAGGGGCCTACCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTTGATTGTt
S45	489	AGTCCTGGCGGGCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTTCTCATGGTGG
		AGTECTGGCGGGCCTACCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTCTGATTGTG
US6	489	AGTCCTGGCGGGCTTGCTACTATTCCATGGTGGGGAACTGGGCTAACGTTCTCATGTGTGG
		AGTECTOGCOGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTTCTGATTGTG
HK4	489	AGTCCTaGCGGGCCTTGCtTACTATTCCATGGTGGGGAACTGGGCAAGGTTTTCATTGTC
		AGICCI AGCGGGCC I IGCCTACTATTCCATGGTGGGGAACTGGGCCAAGGTTTTGATTGTG
P10	489	AGTCCTGGCGGGCCTTGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTGTTGATTGTG
		AGICE IGGEGGGCE I IGCE IACTATTCCATGGTGGGGAACTGGGCTAAGGTCTTGATTGTG
S9	489	AGTCCTGGCGGGCCTcGCCTACTATTCCATGGTGGGGAACTGGGCTAAGGTtTTGATTGTG
		THE TOTAL PROPERTY OF THE PROP
consensus		agTCCTgGCGGGCCTtGCcTACTAtTCCATGGtgGGgAACTGGGCtAAGGTttTgATTGTg
	DK1 T10 D3 D1 HK5 HK8 HK3 T3 SW2 IND8 IND5 SA10 S45 US6 HK4 P10 S9	DK1 489 T10 489 D3 489 D1 489 HK5 489 HK5 489 HK3 489 T3 489 SW2 489 IND8 489 IND5 489 SA10 489 SA10 489 SA5 489 US6 489 HK4 489 P10 489 S9 489

SEO ID NO	<u>: Isolate</u>	
11	DK1	550 tTGCTACTCTTTGCCGGCGTTGATGGG
24	T10	550 ATGCTACTCTTTGCCGGCGTTGATGGG
10	. D3	550 ATGCTACTCTTTGCTGGCGTcGACGGC
9	D1	550 ATGCTACTCTTTGCTGGCGTTGACGGC
14	нк5	550 ATGCTACTETTTGCCGGCGTTGATGGG
15	нкв	
12	нкз	550 ATGCTACTETTTGCCGGCGTTGATGGG
23	Т3	550 CTGCTACTCTTTGCCGGCGTTGATGGG
22	SW2	550 ATGCTACTCTTTGCtGGCGTTGACGGG
17	IND8	
16	IND5	111111111111111111111111111111111111111
21	SA10	
	SAIU	550 ATGCTACTCTTTGCCGGCGTTGACGGG
20	S45	550 ATGCTACTCTTTGCCGGCGTTGACGGG
25	US6	550 tTGCTACTCTTTGCCGGCGTTGACGGG
13	HK4	550 ATGCTACTCTTTGCCGGCGTTGACGGG
18	P10	
19	S9	
9-25	consensus	aTGCTACTCTTTGCcGGcGTtGAcGGg

# FIGURE 1C

SEO ID NO	: <u>Isolate</u> T2	1 GCcCAAGTGAGGAACACCAgccgCgGtTACATGGTGACtAACGACTGTTCcAATGAGAGCr
27	Т4	1 GCaCAAGTGAAGAACACCACTACACGTACATGCGTGACAACACACAC
28	Т9	1 GCCGAAGTGAAGAACACCAGTACCAGCTACCATGGTGACCAACGACTGTTCEAATGACAGCA  1 GCCGAAGTGAAGAACACCAGTACCAGCTACATGGTGACAAATGACTGTTCCAACGACAGCA
29	US10	
26-29	consensus	GcccAAGTGAagAACACCAgtacCaGcTAcATGGTGACcAA-GACTGtTCcAA-GACAGCA
SEO ID NO	: <u>Isolate</u> T2	62 TCACcTGGCAGCTCCAAGCCGCGGTtCTCCACGTCCCCGGGTGTATCCCGTGtGAGAggct
27	<b>T4</b>	
28	Т9	62 TCACCTGGCAACTCCAGGCCGCGGTCCTCCACGTCCCGGGTGCGTGC
29	US10	
26-29	consensus	TCAC-TGGCA-CTccAgGCcGCGGTcCTCCACGTcCCCGGGTGtgTCCCGTGcGAGA-agt
SEO ID NO:	<u>Isolate</u>	
26	T2	123 GGGAAATACATCCCGATGCTGGATACCGGTCaCACCAAACGTGGCCGTGCGGCAGCCCGGC
27	T4	123 GGGAAATACATCtCGGTGCTGGATACCGGTtTCACCAAACGTGGCCGTGCGGCAGCCCGGC
28	Т9	123 tGGAAAcgCgTCgCGGTGCTGGATACCGGTCTCgCCAAACGTaGCtGTGCAGCGGCCTGGC
29	US10	123 gGGAAAtaCaTCtCGGTGCTGGATACCGGTCTCaCCAAAtGTgGCcGTGCAGCGGCCTGGC
26-29	consensus	gGGAAAtaCaTCtCGgTGCTGGATACCGGTctCaCCAAAcGTgGCcGTGC-GC-GCC-GGC
SEO ID NO:	<u> Isolate</u>	
26	T2	184 GCtCTtACGCAGGGCTTGCGGACGCACATcGACATGGTTGTGATGTCCGCCACGCTCTGCT
27	T4	184 GCCCTCACGCAGGGCTTGCGGACGCACATEGACATGGTTGTGATGTCCGCCACGCTCTGCT
28	. <b>T</b> 9	184 GCCCTCACGCAGGCCTTGCGGACGCACATCGACATGGTTGTGATGTCCGCCACGCTCTGCT
29	US10	184 GCCTCACGCAGGCTTGCGGACLCACATCGACATGGTCGTGATGTCCGCCACGCTCTGCT
26-29	consensus	GCcCTcACGCAGGGCTTGCGGACGCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT
SEO ID NO:	<u> Isolate</u>	
26	T2	245 CTGCcCTcTACGTGGGGGACCTCTGCGGGGGGGGGGTGATGCTCGCAGCCCAGATGTTCATtGT
27	T4	245 CTGCTCTtTACGTGGGGGACCTCTGCGGGGGGGTGATGCTCGCAGCCCAGATGTTCATcGT
28	Т9	245 CCGCTCTcTACGTGGGGGAtCTCTGCGGCGGGGGTaATGCTCGCcGCtCAGATGTTCATTaT
29	US10	245 CCGCTCTtTACGTGGGGGActTCTGCGGtGGGaTgATGCTCGCaGCcCAaATGTTCATTgT
26-29	consensus	C-GCtCT-TACGTGGGGGAccTCTGCGGcGGGGTgATGCTCGCaGCcCAgATGTTCATtgT

# FIGURE 1C

SEO ID NO 26 27 28 29 26-29	: Isolate T2 T4 T9 US10 consensus	306 CTCGCCGCgACGCCACTGGTTTGTGCAAGAATGCAATTGCTCcATCTACCCCGGLACCATC
SEO ID NO 26 27	: <u>Isolate</u> T2 T4	367 ACTGGACACCGTATGGCATGGACATGATGAACTGGTCGCCCACAGCCACCATGATCC
28 29	Т9	367 ACTGGACACCGTATGGCATGGACATGATGATGAACTGGTCGCCCACaaCCACCATGATCt
26-29	US10 consensus	367 ACCGGGCACCGTATGGCATGGGACATGATGATGACTGGTCGCCCACggCCACttTGATCc  ACtGGaCACCGTATGGCATGGGACATGATGATGACTGGTCGCCCAC-gCCACcaTGATCc
SEO ID NO:	<u>Isolate</u> T2	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCATCaTAGACATCaTcgGCGGGGCtCACTGGGG
27	T4	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCATCLTAGACATCGTLAGCGGGGCCaCACTGGGG
28	Т9	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCATCATGACATCATCAGCGGAGCtCACTGGGG
29	US10	428 TGGCGTACGEGATGCGCGTTCCCGAGGTCATCATAGACATCATEAGCGGGGCGCAETGGGG
26-29	consensus	TGGCGTACGcGATGCGCGTTCCCGAGGTCATCaTAGACATCaT-aGCGGGGCtCAcTGGGG
SEO ID NO: 26 27	Isolate T2	489 CGTCATGTTtGGCTTGGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAGGTCATTGTCATC
28	Т9	489 CGTCATGTTCGGCCTACCTTCTCTATGCAGGGAGCGTGGGCGAAAGTCGTTGTCATC
29	US10	489 CGTCtTGTTCGGCCTAGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAAGTCGTTGTCATC
26-29	consensus	CGTCaTGTTcGGCtT-GCCTACTTCTCTATGCAGGGAGCGTGGGCGAA-GTCgTTGTCATC
SEO ID NO:	<u>Isolate</u> T2	550 CTetTGCTGGCtGCTGGGGTGGACGCG
27	T4	550 CTECTGCCGCTGGGTGGACGCG
28	Т9	550 CTgtTGCTcaCCGCTGGcGTGGACGCG
29	US10	550 Citerigitagiciocitos gorios de la companya del companya del companya de la companya del companya della comp
26-29	consensus	CTt - TGCTggCcGCTGGgGTGGACGCG

### FIGURE 1D

SEO ID NO 33 30 32 31 30-33	DK8  DK1  DK11  Consensus	1 GTGGAAGTŁAGAACACCAGTTŁŁAGCTACTACGCCACCAATGATTGCTCGAACAACAGCA
SEO ID NO	: <u>Isolate</u> T8	62 TCACCTGGCAGCTCACCAACGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
30	DK8	62 TCACCTGGCAACTCACCGACGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTCAGAATGA
32	SW3	62 TCACCTGGCAACTCACCACGCAGTCCTCCACCTTCCCGGATGCGTCCCGTGTGAGAATGA
31	DK11	62 TCACCTGGCAACTCACCACGCAGTtCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
30-33	consensus	TCACCTGGCAaCTCACCaACGCAGTtCTCCACCTTCCCGGATGCGTCCCaTGTGAGAATGA
SEO ID NO	<u> Isolate</u>	
33	Т8	123 CAATGCCACCTTGCGCTGCATACAGTaACACCTAATGTGGCTGTGAAACACCGtGGC
30	DK8	123 CAATGCACCCTGCGCTGCATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC
32	SW3	123 tAATGCACCCTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC
31	DK11	123 CAATGGCACCTGCACTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGCGGC
30-33	consensus	CAATGGCACCCTGC-CTGCTGGATACAAGTGACACCTAATGTGGCTGTGAAACACCGcGGC
SEO ID NO:		
33	T8	184 GCACTCACACCTGCGAACGCAtGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
30	DK8	184 GCACTLACTCALAACCTGCGAACACGTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
32	SW3	184 GCGCTCACTCACAACCTGCGAGCACACGTCGATATGATCGTAATGGCAGCTACGGTCTGCT
31	DK11	184 GCaCTCACTCACAACCTGCGAGCACAtaTaGATATGATtGTAATGGCAGCTACGGTCTGCT
30-33	consensus	GCaCTcACTCAcAACCTGCGA-CaCA-gTcGATCATcGTAATGGCAGCTACGGTCTGCT
SEO ID NO:	<u>Isolate</u> T8	245 CGGCCTTGTATGTGGGGGACGTgTGCGGGGCCGTGATGATaGcGTCGCAGGCTtTCATAAT
30	DK8	
32 ·	SW3	245 CGGCCTTGTATGTGGGAGACATGTGCGGGGCCGTGATGATCGTGTCGCAGGCTCTCATAAT
31	DK11	245 CGGCCTTGTATGTGGGAGACgTGTGCGGGGCCGTGATGATCGTGTCGCAGGCTTTCATAgT
30-33	consensus	CGGCCTTGTATGTGGGAGACgTgTGCGGGGCCGTGATGATcGtGTCGCAGGCTtTCATAaT

# FIGURE 1D

SEO ID NO	: <u>Isolate</u> T8	206 NEGGGGGANAGGGANAGAN AND AND AND AND AND AND AND AND AND A
		306 ATCGCCaGAACGCCACAACTTcACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
30	DK8	306 ATCGCCEGAACGCCACAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
32	SW3	306 ATCGCCAGAACGCCACAACTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCGTATC
31	DK11	306 ATCGCCAGAACACCACCACTTTACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCaCATC
30-33	consensus	ATCGCCaGAACgCCACaACTTtACCCA-GAGTGCAACTGTTCCATCTACCAAGGTCatATC
SEO ID NO:	Isolate T8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTGAACTGGTCACCAACTCTCACCATGATCC
30	DK8	367 ACCGGCCACGCATGGCATGGCACGATGCTAAACTGGTCACCAACTCTTACCATGATCC
32	SW3	367 ACCGGCACCGCATGGCGTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
31	DK11	367 ACCGGCCACCGCATGGCATGGATGCTLAACTGGTCACCAACTCTCACCATGATCC
30-33	consensus	ACCGGCCACCGCATGGCaTGGGACATGATGCTaAACTGGTCACCAACTCT-ACCATGATCC
CEO ID NO.	T1	
SEO ID NO:	<u>Isolate</u> T8	428 TCGCCTAcGCtGCTCGTGTGCCTGAaCTAGtCCTtgAaGTTGTCTTCGGCGGCCATTGGGG
30	DK8	428 TCGCCTATGCCGCTCGTGTTCCTGAGCTAGCCCTccAgGTTGTCTTCGGCGGCCATTGGGG
32	SW3	428 TEGCCTATGCCGCTCGTGTTCCTGAGCTAGTCCTTGAAGTTGTCTTCGGCGGCCATTGGGG
31	DK11	428 TEGECTATGCCGCECGTGTTCCTGAGCTAGTCCTTGAAGTCGTCTTCGGtGGtCATTGGGG
30-33	consensus	Tegectaegeegetegteectgagetageectegaagtegtettegegegecattgggg
SEO ID NO:	<u>Isolate</u>	
33	T8	489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAaGGAGCGTGGGCCAAAGTCATcGCCATC
30	DK8	489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAGGGGCGTGGGCCAAAGTCATTGCCATC
32	SW3	489 CGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAAGGAGCGTGGGCCAAGGTCATTGCCATC
31	DK11	489 tGTGGTGTTTGGCTTGGCCTATTTCTCCATGCAGGGAGCGTGGGCCAAGGTCATTGCCATC
30-33	consensus	cgtggtgtttggcttggcctatttctccatgca-ggagcgtgggccaa-gtcattgccatc
SEO ID NO:	<u>Isolate</u> T8	550 CTCCTcCTTGTCGCAGGAGTGGAcGCA
30	DK8	
32	SW3	
31	DK11	
30-33	consensus	CTCCTtCTTGTcGCAGGAGTGGAtGCA

### FIGURE 1E

SEO ID	NO: <u>Isolate</u> DK12	1 tTAGAGTGGCGGAATGTGTCCGGCCTCTACGTCCTTACCAACGACTGTtCCAATAGCAGTA
36	HK10	1 CTAGAGTGGCGGAATGTGTCTGGCCTCTATGTCCTACCAACGACTGTCCCAATAGCAGTA
37	S2	1 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTCACCAACGACTGTTCCAATAGCAGTA
. 39	S54	1 CTAGAGTGGCGGAATACGTCTGGCCTCTATaTCCTTACCAACGACTGTTCCAATAGCAGTA
38	S52	1 CTAGAGTGGCGGAATACGTCTGGCCTCTATGTCCTTACCAACGACTGTTCCAATAGCAGTA
35-39	consensus	CTAGAGTGGCGGAATaCGTCLGGCCTCTALGTCCTLACCAACGACTGTLCCAATAGCAGTA
SEO ID	NO. Toologo	
35	NO: <u>Isolate</u> DK12	62 Tegtgtatgaggecgatgacgtcattctgcacacacctggctgtgtaccttgtgttcagga
36	HK10	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACCCTGGCTGTGTACCTTGTGTTCAGGA
37	S2	62 TTGTGTATGAGGCCGATGACGTLATTCTGCACACACCTGGCTGTACCTTGTGTTCAGGA
39	S54	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACCCCGGCTGTGTACCTTGTGTTCAGGA
38	S52	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACCCCGGCTGTGTACCTTGTGTTCAGGA
35-39	consensus	TEGTGTATGAGGCCGATGACGTCATTCTGCACACCCEGGCTGTGTACCTTGTGTTCAGGA
SEO ID	NO: Isolate	
35	DK12	123 CGGCAATACATCLACGTGCTGGACCTCAGTGACGCCTACAGTGGCAGTCAGGTACGTCGGA
36	HK10	123 CGGCAATACATCCACGTGCTGGACCTCgGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
37	S2	123 CGGLAATACATCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAGGTALGTCGGA
39	S54	123 CGGCAATACATCCACGTGCTGGACCCCAGTGACACCTACGGTGGCAGTCAGGTACGTCCCA
38	S52	123 CGGCAATACATCCAtGTGCTGGACCCCAGTGACACCTACGGTGGCAGTCAGGTACGTCGGA
35-39	consensus	CGGCAATACATCCACGTGCTGGACCCCAGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
SEO ID 1	NO. Isalasa	·
35	NO: <u>Isolate</u> DK12	184 GCAACCACCGCETCGATACGCAGTCATGTGGACCTGCTAGTGGGCGCGGCCACGATGTGCT
36	НК10	184 GCAACCACCGCCTCGATACGCAGTCATGTGGACCTCTTAGTGGCCCCCCGCAGGCCCCCCAGGCCCCCCCC
37	S2	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTGGTGGGCGCGGCCACtATGTGCT
39	S54	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT
38	S52	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTATTAGTGGGCGCGGCCACGCTGTGCT
35-39	consensus	GCAACCACCGCtTCGATACGCAGTCATGTGGACCTatTaGTGGGCGCGGCCCACgaTGTGCT

# FIGURE 1E

SEO ID			
35	DK12	245	CTGCGCTCTACGTGGGGtGATgTGTGTGGGGCCGTCTTCCTtGTGGGACAAGCCTTCACGTT
36	HK10	245	CIGCGCICIACGTGGGCGATATGTGTGGGGGCCGTCTTCCTCGTGGGACAAGCCTTCACGTT
37	. S2	245 (	
39	S54	245 (	CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTCTCGTGGGACAAGCCTTCACGTT
38	S52		
35-39	consensus		CTGCGCTCTAcGTGGGLGATaTGTGTGGGGCCGTCTTLCTcGTGGGACAAGCCTTCACGTT
600 TD			
SEO ID	NO: Isolate DK12	306 (	CAGACCECGTCGCCATCAAACAGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAECTT
36	HK10	306 (	CAGACCGCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCACCTT
37	S2	306 C	CAGACCTCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
39	S54	306 (	AGACCTCGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
38	S52	306 0	
35-39	consensus	c	PAGACCECGTCGCCATCAAACgGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAEcTT
SEO ID	NO: Isolate		
35	DK12	367 T	CAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCLGTGGGTATGGTGG
36	HK10	367 I	
37	S2	367 T	
39	S5 <b>4</b>	367 <b>T</b>	CAGGACATCGAATGGCTTGGGATATGATGATGATTGGTCCCCGCTGTGGGTATCCTCC
38	S52	i	
35-39	consensus	T	CAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCLGTGGGTATGGTGG
SEO ID	NO. Isalana		
35	NO: <u>Isolate</u> DK12	428 T	AGCGCACGTCCTGCGtcTGCCCCAGACCTTGTTCGACATAATAGCtGGGGCCCATTGGGG
36	НК10	428 T	GGCGCACGTCCTGCGGTTGCCCCAGACCTTGTTCGACATAATAGCCGGGGCCCATTGGGG
37	S2	1	GGCGCACGTtCTGCGtTTGCCCCAGACCGTGTTCGACATAATAGCCGGGGCCCATTGGGG
39	S54	428 1	GGCGCACATCCTGCGATTGCCCCAGACCTTGTTTGACATACTGGCCGGGGCCCATTGGGG
38	S52		GGCGCACATCCTGCGATTGCCCCAGACCTTGTTTGACATACTGGCCGGGGCCCATTGGGG
35-39	consensus	T	gGCGCACgTcCTGCG-tTGCCCCAGACCtTGTTcGACATAaTaGCcGGGGCCCATTGGGG

#### FIGURE 1E

SEO ID	NO: Isolate		
35	DK12	489	CATCATGGCGGGCCTAGCCTATTACTCCATGCAGGGCCAACTGGGCCAAGGTCGCTATCATC
36	HK10	489	CATCTTGGCaGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
		•	
37	S2	489	CATCTTGGCGGCCTAGCCTATTACTCCATGCAGGCCAACTGGGCCAAGGTCGCTATCATC
20			
39	S54	489	CATCTTGGCGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
38	050		
38	S52	489	CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATtgTC
35-39	consensus		-
33 33	COMBENIAUS		CATCTTGGCGGGCCTAGCCTATTACTCCATGCAGGGCCAACTGGGCCAAGGTCGCTATCATC
SEO ID			
	NO: Isolate		
35	NO: <u>Isolate</u> DK12	550	ATGGTTATGTTTTCAGG=GTCGATGCC
		550	ATGGTTATGTTTTCAGGaGTCGATGCC
			111111111111111111111111111111
35 36	DK12		ATGGTTATGTTTTCAGGAGTCGATGCC
35	DK12	550	
35 36 37	DK12 HK10 S2	550	111111111111111111111111111111
35 36	DK12 HK10	550 550	
35 36 37 39	DK12 HK10 S2 S54	550 550 550	
35 36 37	DK12 HK10 S2	550 550 550	
35 36 37 39	DK12 HK10 S2 S54	550 550 550 550	

# FIGURE 1F

SEO ID NO: Iso	olate Z7 1	GTCAACTATCACAATGCCTCGGGCGTCTATCACATCACCAACGACTGCCCGAACTCGAGCA
42		
42-43 consensus		GTLAACTATCgCAATGCCTCGGGCGTCTATCACGTCACCAACGACTGCCCGAACTCGAGCA
SEO ID NO: Iso	<u>late</u> 27 62	TAATGTATGAGGCCGAACACCACATCCTACACCTCCCAGGGTGCGTACCCTGTGTGAGGGa
42	<b>Z</b> 6 62	TAGTGTATGAGGCCGAACACCAGATCTTACACCTCCCAGGGTGCLTGCCCTGTGTGAGGGL
42-43 consensus	(26)	TAGTGTATGAGGCCGAACACCAGATCtTACACCTCCCAGGGTGCtTgCCCTGTGTGAGGGt
SEO ID NO: Iso	<u>late</u> 27 123	gGGGAACCAGTCACGCTGCTGGGTGGCCCTTACTCCCACCGTGGCGGCGCCCTTATATCGGT
42		
42-43 consensus	(26)	tGGGAAtCAGTCACGCTGGGTGGCCCTTACTCCCACCGTGGCGGtGtCTTATATCGGT
SEO ID NO: Isol		GCaCCGCTTGAaTCCaTCCGGAGACATGTGGACCTGATGGTAGGCGCtGCTACAGTGTGCT
42	Z6 184	GCTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTGGGCGCCGCTACTGTaTGCT
42-43 consensus	(26)	GCtCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTgGGCGCcGCTACtGTaTGCT
SEQ ID NO: Isol		CcGCtCTCTACaTTGGGGACCTGTGCGGTGGcGtATTtTTGGTTGGtCAGATGTTtTCTTT
42	<b>Z6</b> 245	CtGCCTCTACgTTGGAGAtCTGTGCGGTGGTGCATTCTTGGTTGGCCAGATGTTCTCCTT
42-43 consensus	(26)	CtGCCCTCTACgTTGGaGAtCTGTGCGGTGGtGcATTCTTGGTTGGcCAGATGTTcTCcTT
SEO ID NO: Isol		CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTALGCGGGGCAcgTt
42		
42-43 consensus	(26)	CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCLATCTACGCAGGGCALaTC
SEO ID NO: Isol		ACAGGCCACAGAATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCtTGgTCC
42		
42-43 consensus		ACGGGCCACAGGATGGCATGGGACATGATGATGAACTGGAGTCCCACAACCACCCTGCTtC

# FIGURE 1F

SEO ID NO: 43 42 42-43 conse	<u>Isolate</u> 27 Z6 nsus (Z6)	428	TCGCCCAGGTLATGAGGATCCCTAGCACTCTGGTgGACCTACTCACTGGAGGGCACTGGGC
43 42 42-43 conser	Isolate Z7 Z6 nsus (Z6)	489	taTCCTTaTeGGGGTGGCaTACTTCtGCATGCAAGCTAATTGGGCCAAGGTCATtCTGGTC
SEO ID NO: 43 42 42-43 conser	<u>Isolate</u> 27 26 usus (26)	550	CTTTTCCTCTaCGCTGGAGTTGATGCC

### FIGURE 1G

SEO ID NO			
45	SA1	1	GTtCCCTACCGGAATGCCTCTGGGGTTTAcCATGTCACCAATGACTGCCCAAACTCCTCCA
47	SA5	1	GTCCCCTACCGAAATGCCTCTGGGGTTTATCATGTCACCAATGATTGCCCAAACTCTTCCA
49	SA7	1	GTCCCCTACCGAAATGCCTCcGGGGTTTATCATGTCACCAATGATTGCCCGAACTCTTCCA
46	SA4	1	GTTCCCTACCGAAACGCCTCTGGGGTTTATCATGTCACCAATGATTCCCCAAACGCCTCTGGGGTTTATCATGTCACCAATGATTCCCCAAACGCCAAACGCCTCTGGGGGTTTATCATGTCACCAAATGATTCCCCAAAACGCCTCTGGGGGTTTATCATGTCACCAAATGATTCCCCCAAAACGCCTCTGGGGGTTTATCATGTCACCAAATGATTCCCCCAAAACGCCTCTGGGGGTTTATCATGTCACCAAATGATTCCCCCAAAACGCCTCTGGGGGTTTATCATGTCACCAAATGATTCCCCCAAAACGCCTCTACAAACGCCTCTACAAAACGCCTCTCTCACAAAACGCCTCTCTCACAAAACGCCTCTCACAAAAACGCCTCTCTCACAAAACGCCTCTCACAAAACGCCTCTCACAAAACGCCTCTCACAAAAACGCCTCTCTCACAAAAACGCCTCTCACAAAAACGCCTCTCACAAAAAACGCCTCTCACAAAAAAACGCCTCTCACAAAAAAAA
50	SA13	1	GTTCCCTACCGAAATGCCTCTGGGGTTTATCATGTCACCAATGTCTTCAC
48	SA6		IIII IIII IIIIIIIIIIIIIIIIIIIIIIIIIIII
		1	ĠŦŦĊĊŧŦĂĊĊĠġĂĂŦĠĊĊŦĊŦĠĠĠĠŢġŦĂŦĊĂŦĠŦŧĀĊĊĀĀŦŢĠĊĊĊĀĀĀĊŦĊŢŦĊĊĀ
45-50	consensus		GTECCCTACCGAAAEGCCTCEGGGGTETAECATGTCACCAATGAETGCCCAAACTCETCCA
SEO ID NO:	<u> Isolate</u>		
45	SA1	62	TAGTCTACGAGGCTGATAGCCTGATCTTGCACGCACCTGGCTGCGTGCCCTGTGTCAGGCA
47	SA5		TAGTUTA CAGGUETATA A COTO DE COTO COTO COTO COTO COTO COTO COTO COT
49	SA7		TACTOTAL CACCOTTO
46	SA4		IIII II IIIIIII IIIIIIIIIIIIIIIIIIIIII
			TAGTETACGAGGCTGATAACCTGATCTTGCAEGCACCTGGTTGCGTGCCETGTGTCAGGCA
50	SA13	62	TEGTCTACGAGGCTGATGACCTGATCTTACACGCACCTGGTTGCGTGCCCTGTGTAGGCA
48	SA6	62	TAGTCTALGAGGCTGATGACCTGATCCTACACGCACCTGGCTGCCCTGTGTCCGGAA
45-50	consensus		TAGTCTACGAGGCTGAtaaCCTGATC-TgCACGCACCTGGtTGCGTGCCCTGTGTCaggCA
SEO ID NO:	<u>Isolate</u> SA1	123	AGATA ATCTCA CTA COTTCATOR
47	SA5		AGATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACACTGTCAGCCCCGACCLTCGGA
		123	AGGTAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACATTGTCAGCCCCGAACCTCGGA
49	SA7	123	ABATAATGTCAGTAGGTGCTGGGTCCAAATCACCCCCACATTGTCAGCCCCGAACCTCGGA
46	SA4	123	AGATAATGTCAGTAaGTGCTGGGTCCAAATCACCCCCACGTTGTCAGCCCCGAAtCTCGGA
50	SA13		GGGTAATGTCAGTAGGTGCTGGGTCCAGATCACCCCCACACTGTCAGCCCCGAGCCTCGGA
48	SA6		GGaTAATGTCAGTAGaTGCTGGGTtCAtATCACCCCCACACTaTCAGCCCCGAGCCTCGGA
45-50	consensus		
			agataatgtcagtaggtgctgggtccaaatcacccccaca-tgtcagccccgaacctcgga

# FIGURE 1G

SEO ID NO	: <u>Isolate</u>		
45	SA1	184	GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGAGCTGCtCTCTGC
47	SA5	184	GCGGTCACGGCTCCTCTGCGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGC
49	SA7	184	GCGGTCACGGCTCCTTCGGAGGGCCGTTGACTACCTAGCGGGAGGGGCTGCCCTCTGCI
46	SA4	184	GCGGTCACGGCTCCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGC1
50	SA13	184	GCGGTCACGGCTCCTCTCGGAGGGCCGTTGACTTAGCGGGGGGGCTGCCCTtTGCT
48	SA6	184	GCGGTCACGGCTCCTCTCGGAGGGCCGTTGALTACTTGGCGGGGGGGGCCGCCCTgTGCT
45-50	consensus		GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGAcTACtTaGCGGGaGGGGCtGCcCTcTGCT
SEO ID NO	: Isolate		
45	SA1	245	CCGCACTATACGTCGGCGACGCGTGCGGGGCAGTGTTtcTGGTAGGCCAAATGTTCACCTA
47	SA5	245	CCGCACTATACGTCGGGGACGCGTGCGGGGCAGTGTTCTTGGTAGGCCAAATGTTCACCTA
49	SA7	245	CCGCgCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAGATGTTCAGCTA
46	SA4	245	CCGCaCTATACGTCGGGGACGCGTGCGGGGCAGTGTTTTTGGTAGGCCAAATGTTCACCTA
50	SA13	245	CCGCGTTATACGTCGGAGACGCGTGCGGGGCAGTGTTTTTGGTAGGtCAAATGTTCACCTA
48	SA6	245	CCGCGTTATACGTCGGAGACGtGTGCGGGGCAtTGTTTTGGTAGGcCAAATGTTCACCTA
45-50	consensus		CCGC-CTATACGTCGGGGACGCGTGCGGGGCAGTGTTLLTGGTAGGCCAAATGTTCACCTA
SEO ID NO	Isolate		•
SEO ID NO	: <u>Isolate</u> SA1	306	
			TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45	SA1	306	TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
<b>4</b> 5 <b>4</b> 7	SA1 SA5	306 306	TAGGCCTCGCCAGCATACCACAGTGCAGACTGCAACTGTTCCATTTACAGtGGCCATATC
<b>4</b> 5 <b>4</b> 7 <b>4</b> 9	SA1 SA5 SA7	306 306 306	TAGGCCTCGCCAGCATACCACAGTGCAGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46	SA1 SA5 SA7 SA4	306 306 306 306	TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50	SA1 SA5 SA7 SA4 SA13	306 306 306 306	TAGGCCTCGCCAGCATACCACAGTGCAGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48 45-50	SA1 SA5 SA7 SA4 SA13 SA6 Consensus	306 306 306 306	TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48	SA1 SA5 SA7 SA4 SA13 SA6 Consensus	306 306 306 306 306	TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48 45-50 SEO ID NO:	SA1 SA5 SA7 SA4 SA13 SA6 Consensus Isolate	306 306 306 306 306	TAGGCCTCGCCAGCATACCACAGTGCAGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48 45-50 SEO ID NO:	SA1 SA5 SA7 SA4 SA13 SA6 Consensus Isolate SA1	306 306 306 306 306 367	TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48 45-50 SEO ID NO: 45	SA1 SA5 SA7 SA4 SA13 SA6 Consensus Isolate SA1 SA5	306 306 306 306 306 367 367	TAGGCCTCGCCAGCATACcACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48 45-50 SEO ID NO: 45 47	SA1 SA5 SA7 SA4 SA13 SA6 Consensus Isolate SA1 SA5 SA5	306 306 306 306 306 367 367 367	TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48 45-50 SEO ID NO: 45 47 49	SA1 SA5 SA7 SA4 SA13 SA6 Consensus Isolate SA1 SA5 SA7	306 306 306 306 306 367 367 367	TAGGCCTCGCCAGCATACCACAGTGCAGGACTGCAACTGTTCCATTTACAGtGGCCATATC
45 47 49 46 50 48 45-50 SEO ID NO: 45 47 49 46 50	SA1 SA5 SA7 SA4 SA13 SA6 Consensus Isolate SA1 SA5 SA7 SA4 SA13	306 306 306 306 306 367 367 367 367	TAGGCCTCGCCAGCATACcACaGTGCAGGACTGCAACTGTTCCATTTACAGTGGCCATATC

#### FIGURE 1G

SEO ID NO: 45 47	Isolate SA1 SA5		TGGCCCAGaTGCTACGGATcCCCCAgGTGGTCATaGACATCATaGCCGGGGGCCACTGGGG
49	. SA7	428	TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
46	SA4	428	TGGCCCAGTTGCTACGGATTCCCCAGGTGGTCATCGACATCATTGCCGGGGGCCACTGGGG
50	SA13	428	TGGCCCAGTTGTTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGCCCACTGGGG
48	SA6	428	TGGCCCAaaTGcTACGGATTCCCCAGGTGGTCATTGACATCATTGCCGGGGGCCACTGGGG
45-50	consensus		TGGCCCAgtTGcTACGGATtCCCCCAgGTGGTCATtGACATCATtGCCGGGGGCCACTGGGG
SEO ID NO:	<u>Isolate</u> SA1	489	GGTCTTGTT+GCCGCCCCTTACTT+GGCTC-GG
47	SA5		GGTCTTGTTtGCCGCCGCATACTTtGCGTCgGCcGCcAACTGGGCTAAGGTAGTGCTGGTt
49	SA7		
46	SA4	489	GGTCTTGTTtGCCGCCGCATATTTCGCGTCAGCGGCTAACTGGGCTAAGGTTaTaCTGGTC
50	SA13	489,	GGTCTTGTTCGCCGCGCATACTACGCGTCGGCGGCTAACTGGGCCAAGGTTGTGCTGGTC
48	SA6	489 (	GGTCTTGTTCGCCGCtGCATACTtCGCGTCGGCGGCTAACTGGGCtAAGGTTGTGCTGGTC
45-50	consensus	(	GGTCTTGTTeGCCGeeGCATAcTteGCGTC-GCgGCtAACTGGGCtAAGGTtgTgCTGGTe
SEO ID NO:	<u>Isolate</u>		
45	SA1	550 (	CTGTT-CCTGTTTGCGGGGGTCGATGGC
47	SA5	550	TIGTTTCTGTTTGCGGGGGTCGATGGC
49	SA7	550 1	TIGHTTCTGTTTGCGGGGTCGATGCC
46	SA4	550	TGTTTCTGTTTGCGGGGTCGATGCC
50	SA13	550 c	TGTTTCTGTTTGCGGGGGTCGATGCC
48	SA6	550 t	TGTTTCTGTTTGCGGGGGTtGATGCC

-TGTTtCTGTTTGCGGGGGTcGATGcC

45-50

consensus

### FIGURE 1H

SEO ID N 30-33 34 26-29 35-39 9-25 1-8 40 42-43 44 41 45-50 51	(IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a) (4a) (4c) (4d) (4b) (5a)	1 1 1 1 1 1 1	GCCAAC CTAGAG CTAGAG LACCAAC GAGCAC GTLAAC TACAAC GTGCAC GTLCC	GTCAGGAACAt GTCAAGGACAC GTGAAGAACAC GTGCGCAACTC GTGCGCAACTC GACCGCAATGC GACCGCAACGC GACCGCAACAC GACCGCAACAC GACCGCAACAC GACCGCAACAC GACCGCAACAC GACCGCAACCC GACCGCAACCC GACCGCAACCC	CGGCGACTI CAGTACCA GTCTGGCC GTCCGGGGG TTCGGGCA CTCGGGGG TTCGGGGG TTCGGGGG TTCGGGGG TTCGGGGG TTCGGGGGG TTCGGGGGG	CCTAC GCTAC FCTAC FCTAC FCTAT FCTAC FCTAC FCTAC	ATGCC( ATGGT( gTCCT) cAtGT( CATGT( CACAT( CACAT( CACGT( CATGT( CA	BAC BAC BAC BAC BAC BAC BAC BAC BAC BAC	CAA CAA GAA CAA CAA CAA CAA	CGA CGA CGA TGA TGA CGA TGA	TTG CTG CTG CTG CTG CTG TTG CTG	CTC tTC CTC CCC CCC CCC	CAA CAA CAA TAA GAA GAA TAA	CTCTAG LEGACAG TAGCAG CTCAAG CTCGAG TTCCAG CTCGAG CTCGAG CACCAG	TAA BAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
1-51	consensus			A		TA		AC	AA	GA	TG	С	AA		
SEO ID N	O: Genotype														
30-33	(IV/2b)	62	TONCOM	CC2 - CTC2 - C											
34	(1V/2B) (2c)	62	TCACCTG	GCAACTCACC	ACGCAGT	CTCC	ACCTTC	CCC	GA?	rgc	GTC	CCa?	TGT	GAGAATO	iΑ
26-29	(III/2a)		TCGITIC	CACCITGAAC	GAGCAGTC	لاسلملين	חדים מידינ	مكسر	בת בתב			~~~	$n \sim m$	~~~~	
35-39	(V/3a)	62	TUNCCIO	GCMGC I CCMGC	CCGCGGTC	CTCC	ላርርጥራር	יררנ	בככיו	PC:+ 4	~~~	7000	ma -	~~~~	
9-25	(II/1b)	02	TCGIGIA	ことをコープリングルント	ACGICATI	יייבאורי).	יעטעטנ			$r \sim r \sim$	~~~ ~	7000	~~~		1
1-8	(I/1b) (I/1a)	02	1001019	CONGOCAGCOC	ACATGATC	ATGC	7 こり こくて	$\cdot$	3/2/~7	rc~	~~~		<b>7</b> ~~	~~~~~	
40	(1/1d) (4a)	~-			MIGCAIC		7CS(.E(.		~	~~~	~~/	~~~			
42-43	(4c)	62	*****	TOWNOL TONCE	ATCACATO	CTIACY	ا کالملکات	CCC	יככי	$\mathbf{r}$	יעידיב	~~~	r	~~~ ~ ~~ -	_
44	(4C) (4d)	<b>0</b> 2	TAGIGIA	TOMOGCCGHAC	ACCADATO	יים איוים:	ירושיירירי	יראכ		$\sim$		7~~		~~~~~	
41	(4b)	0.2	TWGICIN	TOWNICCONTI	ACCACATO	ביו מיודו			די תייתי	~~~	THE PARTY AND PROPERTY AND PROP	3	200	~~~~~	
45-50	(4D) (5a)	٠.	TAGIGIA	JOHODIOMORO	ACCACATO	$\mathbf{A}\mathbf{T}\mathbf{G}\mathbf{C}\mathbf{A}$	ا کالملک ا	ראה	יככיז	$\gamma_{\rm CTC}$	マサイノ	J ( )		~~~~~	_
43°50 51	(5a) (6a)	02	TOOTCIN	EJADI JUUNDA	ACCITATO	ידימרים		-	・ヘーベ	~~~	7000	<b>10-5</b>		~~	_
	(64)	62	TUGTGUT	GGAGGCGGATG	CTATGATC	TTGCA	TTTGC	CTG	GAI	GCI	TG	CTI	rgr	TGAGGG	T
1-51	consensus		T	A	T	T CA	C	C G	G I	G	T	:C 1	rg (	3	
SEO ID NO	: Genotype														
30-33	(IV/2b)	1 22	~~~~~	NCC~#CC~~~	<b>~</b> ~~~~~~										
34	(2c)	122	CCCCVVC	ACCCTGCGCTG	CIGGATAC	AAGTg	ACACC	TAA	TGT	GGC	TGI	GAA	<b>LAC</b>	ACCGcGG	С
26-29	(III/2a)			OTCICIONIG	TIGGGIGG	C:(+(+) -1)	A:C.C.C.	ממח	TT	ירכר	יי תייי	" " " " "	·m~ ·	1 2 CC	_
35-39	(V/3a)	+20	goomac	acaicicigii	CIGGATAC	CCCTC	+CaCC	מממ	~~~	`~^~	<b>~~</b> ~	~~~	~~		_
9-25	(II/1b)			MCMI CONCOIG	CIGGACCC	CaGTG	ACACC	דאכי	3 CT	$\sim$	マスペイ	~~~	m		_
1-8	(I/la)	123	gaacaac	rcciccocic	CIGGGIAG	CGCTC	aCtCC	$rac{1}{2}$	$\sim$	~~~		-20	~~ -		_
40	(1/1d) (4a)		OUG FAAC	accrcawdd 10	1113661160	e Gorie	acccc	ראר	$\sim CT$	~~~	マスト	-20	~~~		_
42-43	(4c)		TOGGANG	4041CGCG11G	CITTICACT			TNC	ידים ע	$\sim$	***	~~~		~~~~~	_
44	(4d)		COCONTIC	THE THREE LIGHTS	LIGGIGG	CCCTT	'A כידיריריני	ראכי	CCT	YC.C.C		~~~		mamaaa	
41	(4b)			~~~ 1 C T W C W T (2)		-14 -14	ACCCC	- אר	-	~~~	$\sim$	~~~			_
45-50	(5a)	123	COMOMNIA	4C11C1CGC1G	CIGGGIGC	COLLEC	ACCCC	~אמ~	مدتك			~~~	~~~	maaa	_
51	(6a)		againai	or CHG THGGIG		$\Delta A \Delta T C$	ልሮሮሮሮ	~~~	2 - T	~~~	יא ריר	~~~	~ -		_
	(04)	143	CGAIGAT(	CGTCCACCTG	TGGCATG(	TGTG.	ACCCCC	CAC	CCI	GGC	CAT	ACC	AAA	TGCTTC	a I
1-51	consensus				TGG	T	с сс		т						

# FIGURE 1H

CEO TO NO			
SEO ID NO 30-33			
30-33	(IV/2b)	184	GCaCTCACTCACAACCTGCGAaCaCALgTcGAcaTGATcGTAATGGCAGCTACGGTCTGCT
26-29	(2c) (III/2a)	T 0 4	GUTUTUAUTAAGGGCCTGCGAGCACATCGATATCATCGTGATGTCTGCTACCCTCTCTT
35-39	(TII/2a) (V/3a)	184	GCcCTcACGCAGGGCTTGCGGACGCACATCGACATGGTtGTGATGTCCGCCACGCTCTGCT
9-25		184	GCAACCACCGCETCGATACGCAGTCATGTGGACCTAETAGTGGGCGCGGCCACGATGTGCT
1-8	(II/1b) (I/1a)	184	TUCUCACTACGACAATACGACGCCACGTCGAtTTGCTCGTTCGCCCCGCTcattTTCTCca
40	(1/14) (4a)	184	UTCCCCCCAACGCACCTCCACACACACCCCCCCCCCCCCC
42-43	(4c)	704	· GCTCCGCTTGAGTCGTTCCGGCGACATGTGGACTTAATGGTAGGCGCGCCACTTCTTT
44	(4d)	. T 0.4	GUEUUGUTTGACTUUCTUUGGAGACATGTGGACCTGATGGTGGGCGCGCGCTAC+GT=TGCT
41		184	GUTUUGUTTGAGTUTTGAGAUGTCACGTGGATCTGATGGTGGGCGCGCCCACTCTCTCTCT
45-50	(4b) (5a)	184	GCACCGTTAGAGTCCATGCGCAGGCATGTAGACCTGATGGTGGGTG
51	(6a)	184	GCGGTCACGGCTCCTCTTCGGAGGGCCGTTGACTACtTaGCGGGaGGGGCtGCcCTcTGCT
<b>J1</b>	(64)	184	ACGCCCGCAACGGGATTCCGCAGGCATGTGGATCTTCTTGCGGGCCGCCGCAGTGGTTTGCT
1-51	consensus		m 0
	COMBENIE		T G T GA T G GC T TG T
SEO ID NO:	Genotype		
30-33	(IV/2b)	245	CGCCCTTCTATCTCCcacacacacacacacacacacacacacacacacac
34	(2c)	243	CGGCCTTGTATGTGGGGGACGTGTGCGGGGCCGTGATGATCGLGTCGCAGGCTLTCATAAT
26-29	(III/2a)	243	CTGCCTTTATGTGGGGGACGTGTGTGGGGGGCGCTGATGCTGGCCGCTCAGGTCGTCGTCGT
35-39	(V/3a)	243	CCGCtCTtTACGTGGGGGAccTCTGCGGGGGGGGTGATGCTCGCGGCcCAgATGTTCATtgT
9-25	(II/1b)	245	CTGCGCTCTAcGTGGGGCGATATGTGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT
1-8	(I/la)	245	CCGCtATGTAcGTGGGGGAtCTCTGCGGaTCtGTttTCCTcgTcTCcCAGcTGTTCACctT
40	(4a)	245	CGGCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTtCTtGTCGGtCAaCTGTTCACCtT
42-43	(4c)	245	CTGCCTCTATGTTGGGGACCTCTGCGGAGGTGCCTTCCTGATGGGGCAGATGATCACTTT
44	(4d)	245	CtGCCTCTACGTTGGaGAtCTGTGCGGTGGtGCATTCTTGGTTGGCCAGATGTTCTCCTT
41	(4b)	245	CCGCCTCTACATCGGAGACGTGTGTGGGGGGTGTGTTCTTGGTCGGTC
45-50	(5a)	245	CCGCCTTCTACATTGGAGATCTGTGTGGAGGCGTCTTCCTAGTGGGCCAGCTGTTCGACTT
51	(6a)	245	CCGCgcTATACGTCGGGGACGcGTGCGGGGCAGTGTTttTGGTAGGcCAAATGTTCAcCTA
1-51	consensus		CATCCTGTACATCGGGGACCTGTGTGGCTCTCTTTTTTGGCGGGACAACTATTCACCTT C T TA T GG GA TG GG T T CA T
			C TTA T GG GA TG GG T T CA T
SEO ID NO:	Genotype		
30-33	(IV/2b)	306	ATCGCCAGAACGCCACAACTTLACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCaLATC
34	(2c)	306	GTCGCCACAACACCATACGTTTGTCCAGGAATGCAACTGTTCCATATACCCGGGCCGCATT
26-29	(III/2a)	306	CTCGCCGCaaCacCACTgGTTTGTGCAaGAaTGCAALTGCTCCATGTACCCLGGLACCATC
35-39	(V/3a)	306	CAGACCECGTCGCCATCAAACGGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAECTT
9-25	(II/1b)	306	cTCgCCtCGcCggcAtgaGACagtaCAGgAcTGcAAcTGcTCaaTCTATCCcGGcCacgTa
1-8	(I/la)		
40	1-//	306	CTCtCCCAGGCGCCaCTGGACACGCAAGACTGCAAtTGTTCtATCTA+CG-CGGCA+
	(4a)	300	CICCCCAGGCGCCCCCCCACCCCCACCCCCACCCCCACCCCCC
42-43		306	TCGGCCGCGTCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACCCGGCCALATA
42-43 44	(4a)	306 306 306	TCGGCCGCGCCACTGGACCACGCAGGGCTGCAATTGTTCLATCTACCCGGCCALATA TCGGCCGCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCLATCTACGCAGGGCALATC CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACAGACGAGACTACA
42-43 44 41	(4a) (4c)	306 306 306 306	TCGGCCGCGCCACTGGACACCCCAGGACTGCAALTGTTCLATCTALCCCGGCCALATA TCGGCCGCGCCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCLATCTACGCAGGGCALATC CCAACCTCGCCGCCACTGGACCACCCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTCTTCACCACGACATATC
42-43 44 41 45-50	(4a) (4c) (4d)	306 306 306 306 306	TCGCCCAGGCGCCACTGGACAACGCAAGACTGCAAFTGTTCEATCTAECCCGGCCAFATA TCGGCCGCGCTCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTACACAGGACATATC CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAACTGCTCCATCTACCACGGACATATC CCGACCGCCGCCGCCACTGGACCACCCAGGACTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAFAGGACTGCAACTGCTCCATCTATCACAGGCCAFATGCTAGGCCTCCACACTGCAACTGCTCCACTTTTACACTGCTCACTCA
42-43 44 41 45-50 51	(4a) (4c) (4d) (4b) (5a) (6a)	306 306 306 306 306	TCGCCCAGGCGCCACTGGACAACGCAAGACTGCAAFTGTTCEATCTAECCCGGCCAFATA TCGGCCGCGCTCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTACACAGGACATATC CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAACTGCTCCATCTACCACGGACATATC CCGACCGCCGCCGCCACTGGACCACCCAGGACTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAFAGGACTGCAACTGCTCCATCTATCACAGGCCAFATGCTAGGCCTCCACACTGCAACTGCTCCACTTTTACACTGCTCACTCA
42-43 44 41 45-50	(4a) (4c) (4d) (4b) (5a)	306 306 306 306 306	TCGCCCAGGCGCCACTGGACACGCAGGACTGCAAETGTTCEATCTAECCCGGCCAEATA TCGCCCGCGTCGCCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTACACAGGACATATC CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCCGCCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAEACEACGGTGCAACTGCTCCATCTATACAGGCCAEATC TCAGCCCCGCCGTCATTGGACTGTGCAAGACTGCTCCATCTATACAGGCCACGTC
42-43 44 41 45-50 51 1-51	(4a) (4c) (4d) (4b) (5a) (6a) consensus	306 306 306 306 306	TCGGCCGCGCCACTGGACACGCAGGACTGCAALTGTTCLATCTALCCCGGCCALATA TCGGCCGCGTCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCLATCTACGCAGGGCALATC CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCCGCCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCALACLACGGCCACACACTGCTCCATCTATACAGGCCALATC TCAGCCCCGCCGTCATTGGACTGTCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC
42-43 44 41 45-50 51 1-51 SEQ ID NO:	(4a) (4c) (4d) (4b) (5a) (6a) consensus	306 306 306 306 306 306	TCGCCCAGGCGCCACTGGACACGCAGGACTGCAAETGTTCEATCTAECCCGGCCAEATA TCGCCCGCGCGCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGCACTGGACTACGCAGGACTGCAATTGTTCEATCTACGCAGGGCAEATC CCAACCTCGCCGCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCGCACTGGACCACCCAAGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAEACAGGTGCAACTGCTCCATCTATACAGGCCAEATC TCAGCCCCGCCGTCATTGGACTGCCAAGACTGCTCCATCTATACAGGCCACGTC CC CA TG AA TG TC T TA GG T
42-43 44 41 45-50 51 1-51 <u>SEO ID NO:</u> 30-33	(4a) (4c) (4d) (4b) (5a) (6a) consensus <u>Genotype</u> (IV/2b)	306 306 306 306 306 306	TCGGCCGCGTCGCACTGGACACGCAGGACTGCAAETGTTCEATCTAECCCGGCCAEATA  TCGGCCGCGTCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCEATCTACGCAGGGCAEATC CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAETGGACCACCCAGGATTGCAACTGCTCCATCTATACAGGCCAEATC TCAGCCCCGCCGTCATTGGACTGTGCAAGACTGCTCCATCTATACAGGCCACGTC CC CA TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTAACAGGCCACTCCACCACCGCCCACCGCCCACCGCCCCACCGCCCCCCCC
42-43 44 41 45-50 51 1-51 <u>SEQ ID NO:</u> 30-33 34	(4a) (4c) (4d) (4b) (5a) (6a) consensus <u>Genotype</u> (IV/2b) (2c)	306 306 306 306 306 306 306	TCGCCCAGGCGCACTGGACAACGCAAGACTGCAAETGTTCEATCTAECCAGGCCAEATA  TCGCCCGCGTCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCEATCTACGCAGGGCAEATC CCAACCTCGCCGCCACTGGACCACCCAAGACTGCAACTGTTCCATCTACACAGGACATATC CCGACCGCGCGCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAEACEACGAGACTGCAACTGCTCCATCTATACAGGCCACGTC TCAGCCCCGCCGTCATTGGACTGTGCAAGACTGCTACATCTATACAGGCCACGTC CC CA TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCCACGGACACCGCTTGGGACACCGCTTGGGACACCGCTTGGGACACCGCTTGGGACACCGCATGGTCCACCAACTCTTACCATGATCCACGGGACACCGCATGGCTTGGGATATGATGATCCACGGACACCGCATGGCTTGGGATATGATGATCCACGACCCCACTCTTCACCATGATCCACGGGACACCGCATGGCTTGGGATATGATGATCACCACCCAC
42-43 44 41 45-50 51 1-51 <u>SEO ID NO:</u> 30-33 34 26-29	(4a) (4c) (4d) (4b) (5a) (6a) consensus <u>Genotype</u> (IV/2b) (2c) (III/2a)	306 306 306 306 306 306 306	TCGCCCGCGTCGCACTGGACACGCAGGACTGCAAETGTTCEATCTAECCCGGCCAEATA  TCGCCCGCGTCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGCACGCACTGGACTACGCAGGACTGCAATTGTTCEATCTACGCAGGGCAEATC CCAACCTCGCCGCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTGGTCACGTC CCGACCGCGCGGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAEACEACGGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C CA TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC ACGGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCACCAACTCTTACCACGATGCTCCACGGGACACCGCATGGCTCCACGTGCTCCACCATGCTCCACGGGACACCGCATGCGCATGGGACATGATGCTCCACGATGCTCCACGATGCTCCACGGGACACCGTTGGGACATGGTTGATGATGATCCACCATGCTCCACGGGACACCGTTGGGACATGGTGATGATGATGATCCACCATGCTCCACGGGACACCGTTGGGACATGGTTGATGATGATGATCGTCGCCCACGATGCTCCACGATGCTCCACGGGACACCGTTGGGACATGGTTGATGATGATGATGATGATGATCGTCGCCCACGATGCACCATGCTCCACGATGCTCCACGGGACACCGTTTGGGACATGGTTGATGATGATGATGATGATGATGATCACCACCATGCTCCACGGGACACCGTATGGGACATGATGATGATGATGATGATGATGATCACACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACCATGCACACCATCATCATCATCATCATCATCATCATCATCATCA
42-43 44 41 45-50 51 1-51 SEQ ID NO: 30-33 34 26-29 35-39	(4a) (4c) (4d) (4b) (5a) (6a) consensus Genotype (IV/2b) (2c) (III/2a) (V/3a)	306 306 306 306 306 306 367 367 367 367	TICGCCGCGTCGCACTGGACACGCAGGACTGCAAETGTTCEATCTAECCCGGCCAEATA TCGGCCGCGTCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGCACGCACTGGACTACGCAGGACTGCAATTGTTCEATCTACGCAGGGCAEATC CCAACCTCGCCGCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTGGTCACGTC CCGACCGCGCGGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAEAEAEAEGGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C CA TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC ACCGGACACCGCATGGCATG
42-43 44 41 45-50 51 1-51 SEO ID NO: 30-33 34 26-29 35-39 9-25	(4a) (4c) (4d) (4b) (5a) (6a) consensus Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b)	306 306 306 306 306 306 367 367 367 367 367	TCGCCCAGGCGCCACTGGACAACGCAAGACTGCAAETGTTCEATCTAECCGGGCCAEATA TCGGCCGCGCGCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGCGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTACACAGGCCAEATC CCAACCTCGCCGCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTGGTCACGTC CCGACCGCGCGCGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAETGACCACCCAGGATTGCAACTGCTCCATCTATACAGGCCACGTC TCAGCCCCGCCGTCATTGGACTGTCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C CA TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTEACCATGATCC ACGGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCTACCACCATGCTCC ACGGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCTACCACCATGCTCC TCAGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCTGCCCCCCTTGCTCCC TCAGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCGTGCGCCACTGGTCGC TCAGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCCCCCCCC
42-43 44 41 45-50 51 1-51 SEO ID NO: 30-33 34 26-29 35-39 9-25 1-8	(4a) (4c) (4d) (4b) (5a) (6a) Consensus Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a)	306 306 306 306 306 306 367 367 367 367 367	TCGCCCAGGCGCCACTGGACAACGCAAGACTGCAAETGTTCEATCTAECCCGGCCAEATA TCGGCCGCGCGCCACTGGACCACCCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAACCTCGCCCCCCTGGACTACCCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCAACCTCGCCGCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCCGCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCAETAGACCACCCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC TCAGCCCCGCCGTCATTGGACTGTCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C CA TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTEACCATGATCC ACCGGCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCTACCACCATGCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCTACCACCATGCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCTGCCCCCTCCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACCTGCTCCCCCCCC
42-43 44 41 45-50 51 1-51 SEQ ID NO: 30-33 34 26-29 35-39 9-25 1-8 40	(4a) (4c) (4d) (4b) (5a) (6a) consensus Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a) (4a)	306 306 306 306 306 306 367 367 367 367 367 367	TCGCCCAGGCGCCATGGACAACGCAAGACTGCAACTGTTCCATCTACCCGGCCACATATC TCGGCCGCGCGCGCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACTGGCCATATC CCAACCTCGCGCCACTGACCACCCAAGACTGCAATTGTTCCATCTACACAGGCCATATC CCAACCTCGCCCCCCCCCC
42-43 44 41 45-50 51 1-51 SEO ID NO: 30-33 34 26-29 35-39 9-25 1-8 40 42-43	(4a) (4c) (4d) (4b) (5a) (6a) consensus Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a) (4a) (4c)	306 306 306 306 306 306 367 367 367 367 367 367 367	TCGCCCAGGCGCCATGGACAACGCAAGACTGCAACTGTTACCCAGGCCACATTC TCGGCCGCGTCGCACTGGACCACCCAGAGACTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGCGCCACTGGACTACCCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCAACCTCGCCCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCCGCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTAGGTCACGTC TAGGCCTCGCCAGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTAGGTCACGTC TCAGCCCCGCCGTCATTGGACTGTCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C A TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC ACGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTACCACCATGCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTGCTCCCACCATGCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCCACTGGTCGTCG TCAGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCCCCCCGCCTGTGGTATGGTCG CCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCCCCCCCC
42-43 44 41 45-50 51 1-51 SEO ID NO: 30-33 34 26-29 35-39 9-25 1-8 40 42-43 44	(4a) (4c) (4d) (4b) (5a) (6a) consensus Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a) (4a) (4c) (4d)	306 306 306 306 306 306 367 367 367 367 367 367 367	TCGGCCGCGTCGCACTGGACACGCAGGAGTGCAATTGTTCEATCTAECCGGCCAEATA TCGGCCGCGTCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACCCCAAGACTGCAATTGTTCEATCTACACAGGACATATC CCAACCTCGCCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCCGCCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTAGTCACGTC CCGACCGCCGCCGCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTAGTCACGTC TAGGCCTCGCCAGCAETATGACTGTCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C A TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTLACCATGATCC ACGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTACCACCATGCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTGCTCCCACGACTCTCCACCATGCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCCCCCGCCGTGGGTATGGTGG tCAGGTCACCGCATGGCTTGGGALATGATGATGAACTGGTCCCCCCGCCGTGGTATGGTGG ACCGGCCACAGGATGGCATGGGALATGATGATGAACTGGTCCCCCACACCACCACTGCTCC ACGGCCACAGGATGGCATGGGACATGATGATGAACTGGTCCCCCACACCACCACTGCTCC ACGGCCACAGGATGGCATGGGACATGATGATGAACTGGTCCCCCACCACCACCACCTGCTCC ACGGCCACAGGATGGCATGGGACATGATGATGAACTGGACCCCTACCACCACCTCCTCC ACGGCCACAGGATGGCATGGGACATGATGATGAACTGGAGCCCTACCACCACCTCCTCCC ACGGCCACAGGATGGCATGGGACATGATGATGAACTTGAGGCCCTACCACCACCTCCTCCCACAACACCACCACCTCCTCC
42-43 44 41 45-50 51 1-51 SEO ID NO: 30-33 34 26-29 35-39 9-25 1-8 40 42-43 44 41	(4a) (4c) (4d) (4b) (5a) (6a) consensus  Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a) (4a) (4c) (4d) (4b)	306 306 306 306 306 306 367 367 367 367 367 367 367 367	TCGGCCGCGTCGCACTGGACACGCAGGAGTGCAATTGTTCATCTACCCGGCCATATC CCAGCCGCGTCGCCACTGGACCACCCAGGAGTGCAATTGTTCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACCCCAAGACTGCAATTGTTCATCTACACAGGACATATC CCAGCCGCGCCCCCCAGGACTACCCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCCGCCACTGGACCACCCAAGACTGCAACTGCTCCATCTATCCTGGTCACGTC CCGACCGCCGCCGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTGGTCACGTC TAGGCCTCGCCAGCATATGGACTGTCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C A TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC ACGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTGCTCCCACGACCACTGCTCC ACGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTGGTCCC ACGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCCCCCCGCCGTGGGTATGGTGG tCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCCCCCCGCCGTGGGTATGGTGG ACGGGCCACAGGATGGCTTGGGATATGATGATGAACTGGTCCCCCACAGCACCCTTACTACACCACTCTCCCCACGGCCCAAGGACACACCACTGGTTCC ACGGCCACAGGATGGCTTGGGACATGATGATGAACTGGTCCCCCAACACCACCTCTGCTCC ACGGCCACAGGATGGCTTGGGACATGATGATGATGAACTGGTCCCCCACACCACCTCTGCTCC ACGGCCACAGGATGGCTTGGGACATGATGATGAACTGGAGCCCTACCACCACTCTGCTCC ACGGCCACAGGATGGCTTGGGACATGATGATGAACTGGAGCCCCACACCACCTCTGCTCC ACAGGACACAGAATGGCTTGGGACATGATGATGAACTTGAAGCCCCCACTACCACCACCTCGTTCC TCGGGCCACAGGATGGCTTGGGACATGATGATGAATTGAAGCCCCCACTACCACCACCTCGTTCC TCGGGCCACAGGATGGCCTTGGGACATGATGATGATGAATTGAAGCCCCCACTACCACCACCTCGTTCC TCGGGCCACAGGATGGCCTTGGGACATGATGATGATGATGATTGAACTTGAGGCCCCCACTACCACCACCTCCTACCACCACTCTGCTCC TCGGGCCACAGGATGGCCTTGGGACATGATGATGATGATGATGATGACTGAGCCCCCACTACCACCACCTCCTACCACCACTCTGCTCC TCGGGCCACAGGATGGCCTTGGGACATGATGATGATGATGATGATGATGATGATGATGACTTGAGGCCCCACTGCGACGCTTCATACCACCACCTCCTACCACACACCACCTCCTACCACACACCAC
42-43 44 41 45-50 51 1-51 SEO ID NO: 30-33 34 26-29 35-39 9-25 1-8 40 42-43 44 41 45-50	(4a) (4c) (4d) (4b) (5a) (6a) consensus  Genotype (IV/2b) (II/2a) (V/3a) (II/1b) (I/1a) (4a) (4c) (4d) (4b) (5a)	306 306 306 306 306 306 367 367 367 367 367 367 367 367	TCGGCCGCGCCCCCACTGGACAACGCAGGACTGCAACTGTTCATCTACACTGGCCATATC CCAGCCGCGCCCCCCCCCAGGACTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGCCCCCCCCCC
42-43 44 41 45-50 51 1-51 SEO ID NO: 30-33 34 26-29 35-39 9-25 1-8 40 42-43 44 41	(4a) (4c) (4d) (4b) (5a) (6a) consensus  Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a) (4a) (4c) (4d) (4b)	306 306 306 306 306 306 367 367 367 367 367 367 367 367	TCGGCCGCGTCGCACTGGACACGCAGGAGTGCAATTGTTCEATCTAECCGGCCAEATTA TCGGCCGCGTCGCACTGGACCACGCAGGAGTGCAATTGTTCCATCTACACTGGCCATATC CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCEATCTACACGGCGCAEATC CCAACCTCGCCCACTGGACCACCCAAGACTGCAATTGTTCCATCTACACAGGACATATC CCGACCGCGCCGCCACTGGACCACCCAAGACTGCAACTTCCATCTATCCTAGTCACGTC CCGACCGCCGCCGCACTGGACCACCCAGGATTGCAACTGCTCCATCTATCCTAGTCACGTC TAGGCCTCGCCAGCAETATGACTGTCAAGACTGCAACTGCTCCATCTATACAGGCCACGTC CC C A TG AA TG TC T TA GG T  ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTACCACCATGCTCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCCACTGCTCCC ACCGGACACCGCATGGCTTGGGATATGATGATGAACTGGTCCCCCGCCGTGGGTATGGTGG tCAGGACACCGCATGGCTTGGGALATGATGATGAACTGGTCCCCCCGCCGTGGGTATGGTGG ACCGGCCACAGGATGGCATGGGALATGATGATGAACTGGTCCCCCACCACCACCACTCTCC ACGGCCACAGGATGGCATGGGACATGATGATGAACTGGTCCCCCACCACCACCACCACCACCACCACCACCACCACCA

# FIGURE 1H

SEO ID NO: 30-33 34 26-29 35-39 9-25 1-8 40 42-43 44	Genotype (IV/2b) (2c) (III/2a) (V/3a) (II/1b) (I/1a) (4a) (4c) (4d) (4b)	428 428 428 428 428 428	TG Ta' Ta' TC' TC'	GCG GCG TCG GCt GCC GCC	CAGO CAGO CAGO CAGO CAGO CAGO	TCAT	GCGC GCGC GCGg CCGG GAGG GAGG GAGG	GTT aTC aTC GTC ATC	CCGGA CCCCA CCaCA CCGCA CCCAC CCTAG	AGTC AGGTC AGACC AGCC AGCC AGCC AGCC AGC	ATCT ATCA ETGT GTCG ATCT CTGG ATGG	TGGA TAGA TCGA TGGA TCGA TAGA TCGA	CATO CATO CATO CATO CATO CATO	GTT: ATT: ATT: ATT: GTT: ACTC:	ACAG aGCG GCGG GCTGG GCTGG GCTGG	GAGC GGGC GGGC GEGC GEGC GAGC	TCA CCA CCA CCA CCA CCA GCA	TTGGGG TTGGGG TTGGGG TTGGGG TTGGGG TTGGGG TTGGGG
45-50	(5a)	428	TG	GCC	CAgt	TGCT	ACGG	ATE	CCCCA	CTC	בדיהם	THEN	CIIC	'ATEC	7000	3000	TCAC	CTGGGG
51	(6a)	428	TA'	TCT.	AGCA	TCTT	GAGG	GTA	CCTGA	GATT	ייייייי	CGAG	TCTC	יים בה- יים בהיים ב		7000	CCA	TGGGG
1-51	consensus		T	С				T		JAI I	1010	CGAG	T	T		FIGG		TGGGG
SEO ID NO:	Conon																	
30-33	<u>Genotype</u> (IV/2b)	400																
34	(1V/2B) (2c)	489	CG.	rGG:	IGTI	TGGC	TTGG	CCT	ATTTC	TCCAT	rgca ₍	gGGA	GCGT	GGGC	CAA	GTC	ATto	CCATC
26-29	(III/2a)	407	101	LAA.	TGTT	1.000	JICG		ACTTC	TCCAI	CCA	GGGAT	ГССТ	יככככר	יכא אכ	יבידיר	TOC	יישור עיניים וי
35-39	(V/3a)	407	CG	ica.	1611	CGGC	Tag	CCT	ACTTC	TCTAT	CGCA	GGGAC	3CGT	ന്ദ്രവ	- ממסי	CTC	CALAL!	בתר אתים
9-25	(II/1b)	489	CM.			guuc	JIAG	CCII	ATTAC	TCcAT	$\mathbf{r}\mathbf{G}\mathbf{C}\mathbf{A}$	aGGCZ	$T \cap A A$	GGGC	יר א א כ	ישייי	لاملسات	TOTTO
1-8	(I/la)	407	agı		rgec	GGGC	JIEG	CCTZ	ACTAE'	TCCAT	rGG to	aGGaz	יוויי) ע	രഭഭ	ነተ አአር	<u>'C'T'+</u>	+T~7	THE CHIEF
40	(4a)	407	MG 1		1 alc		MAG	CGTZ	$\Delta TTTC$	TCCAT	rgg+(	GGaz	$\Delta \Delta CT$	അവ	ית תבי	CTC	~~~	TO COM
42-43	(4c)	307	CGI		1000	ひいじじょ	17.66	$\mathbf{CGT}$	ACTITIC	AGCAT	TGC A	ひんにしょ	עבע ע	വവാ	יר א איני	(TT)	CMCC	WCCMO.
44	(4d)	409	COI		rigi	TGGGT	TGG	cgr	ACTTC	aGtAI	CA	AGCT	ATT	GGGC	CAAa	GTC	ATCC	TGGTC
41	(4b)	489	VC1			TCCTC	TAG	CGTY	ACTTC	AGCAT	GCA	AGCT	VATT	GGGC	CAAG	GIT	ATCC	TGGTC
45-50	(5a)	489	CCT	. T C 1	1 1 G C	-6616	TAG		CTTC	AGCAI	GCA	SAGTA	AACT	GGGC	GAAG	GTC	ATCC	TGGTC
51	(6a)	489	CAT	יארי	1011	7CCCC		-A17	CLEC	GCGTC	gGC	GCL	ACT	GGGC	'taag	GTt	gTgC	TGGTC
	(00)	103	- CA-1		.AC 1.	AUCCU	1116		ACT TI	GGCAT	GGC	rggcz	ACT	GGCT	'AAAA'	GTT	CTGG	CTGTT
1-51	consensus		1	· 1	r	G	G	Т	T				T	GG	AA	GT		т
SEO ID NO:	<u>Genotype</u>																	
30-33	(IV/2b)	550	CTC	CTt	CIT	GTcGC	'AGG	GTC	GALG	CA								
34	(2c)	550	CTC	CTG	CTG	ACTGC	TGG	GTG	GAGG	CG								
26-29	(III/2a)	550	CTt	tTG	CTq	qCcGC	TGG	GTG	GACGO	CG								
35-39	(V/3a)	550	ATG	gII	'ATG'	TTTTC	AGG	TGTC	GALGO	CC								
9-25	(II/1b)	550	aTG	CTA	CTC	TTTGC	cGGc	GTt	GAcGC	Gar								
1-8	(I/la)	550	CTG	tTG	CTg	TTtqC	CGGC	GTC	:GAtGC	CĞ								
40	(4a)	550	CII	TTC	CIC	MTGC	TGGC	GTA	GACGO	C								
42-43	(4c)	550	CIT	TTC	CIC	rtcgc	TGG	GTI	GATGO	CC								
44 41	(4d)	550	CTG	TTT	CIC	TTGC	TGGA	GTC	GACGO	T								
45-50	(4b)	550	CTA	TTC	CIC	TTGC	CGGG	GTC	GAGGG	3A								
45-50 51	(5a)	550	tTG	TTt	CIG	TTGC	GGGG	GTC	GATG	C:C								
J.1	(6a)	550	CIG	TC	CTA	TTGC	AGGG	GTT	GAAGO	ZA.								

C GG GT GA G

1-51

consensus

T T T

# FIGURE 2A

SEO ID NO:	<u> Isolate</u>	
56	S14	1 YOVRNSTGLYHVTNDCPNSSIVYELADAILHaPGCVPCVREGNLSRCWVAMTPTVATRDGK
52	DK7	1 YOVRNSTGLYHVINDCPNSSIVYEAADAILHTPGCVPCVREGNvSRCWVAMTPTVATRDGK
59	US11	1 YOVRNSTGLYHVINDCPNSSIVYEAADAILHTPGCVPCVREGNASRCWVAMTPTVATRDGK
55	DR4	1 HOVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGNtSRCWVAVTPTVATRDGK
54	DR1	1 HOVRNSTGLYHVTNDCPNSSIVYEAADAILHAPGCVPCVREGNASRCWVAVTPTVATRDGK
53	DK9	1 YQVRNSSGLYHVTNDCPNSSIVYEAADAILHSPGCVPCVREGNASKCWVAVAPTVATRDGK
58	SW1	1 YOVRNSSGLYHVTNDCPNSSIVYETADAILHSPGCVPCVREdgApKCWVAVAPTVATRDGK
57	S18	1 YQVRNStGLYHVTNDCPNSSIVYETADtILHSPGCVPCVREgnAsrCWVpVAPTVATRDGK
52-59	consensus	yQVRNStGLYHVTNDCPNSSIVYEaADaILH-PGCVPCVREgnasrCWVavtPTVATRDGK
SEO ID NO:	<u> Isolate</u>	
56	S14	62 LPatQLRRyIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRR1WTTQdCNCSIYPGHI
52	DK7	62 LPTaQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTQGCNCSIYPGHI
59	US11	62 LPTTOLRRHIDLLVGSATLCSALYVGDLCGSVFLVGOLFTFSPRRHWFTQGCNCSIYPGHI
55	DR4	62 LPTTQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRhHWTTQDCNCSIYPGHI
54	DR1	62 LPTTOLRRHIDLLVGSATLCSALYVGDLCGSVFLVGOLFTFSPRRHWTTODCNCSIYPGHI
53	DK9	62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTQDCNCSIYPGHI
58	SW1	62 LPATOLERHIDLLVGSATLCSALYVGDLCGSVFLVSOLFTFSPRRHWTTODCNCSIYPGHT
57	S18	62 LPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVSQLFTiSPRRHWTTQDCNCSIYPGHI
52-59	consensus	LP-tQLRRhIDLLVGSATLCSALYVGDLCGSVFLVgQLFTfSPRrhWTTQdCNCSIYPGHI
SEO ID NO:	71	
56 56	<u>Isolate</u> S14	123 TGHRMAWDMMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
52	DK7	123 TGHRMAWDMMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
59	US11	123 TGHRMAWDMMNWSPTaALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
55	DR4	123 TGHRMAWDMMNWSPTTALVVAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVLVV
54	DR1	123 TGHRMAWDMMNWSPTTALVMAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVVVV
53	DK9	123 TGHRMAWDMMNWSPTaALVMAQLLRIPQAILDMIAGAHWGVLAGIAYFSMVGNWAKVVVV
58	SW1	123 TGHRMAWDMMNWSPTTALVvAQLLRIPQAVLDMIAGAHWGVLAGIAYFSMVGNWAKVLiV
57	S18	123 TGHRMAWDMMMNWSPTTALViAQLLRvPQAVLDMIAGAHWGVLAGIAYFSMaGNWAKVLlV
52-59	consensus	TGHRMAWDMMNWSPTtalvvaQllripQaildmiagahwgvlagiayfsmvgnwakvlvv

# FIGURE 2A

SEO ID NO	): <u>Isolate</u>		
56	S14	184	LLLFAGVDA
52	DK7	184	LLLFAGVDA
59	US11	184	LLLFAGVDA
55	DR4	184	LLLFAGVDA
<b>5</b> 4			
54	DR1	184	LLLFAGVDA
53	DYO		
53	DK9	184	LLLFtGVDA
58	CWI		
36	SW1	184	LLLFsGVDA
57	S18	3.04	
٠, د	219	184	LLLFaGVDA
52-59	consensus		III D-CIDA
	COMPENDED		LLLFaGVDA

# FIGURE 2B

SEO ID NO:	<u>Isolate</u>	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVfEAaDlIMHTPGCVPCVREGNsSRCWVALTPTLAARNE
60		
62	DK1	1 YEVRNVSGVYHVTNDCSNSSIVYEAVDVIMHTPGCVPCVRENNhSRCWVALTPTLAARNA
CA	7772.4	
64	. HK4	1 hEVhnvsgiyhvindcsnssivyeaadmimhtpgcvpcvrennssrcwvaltptlaarna
76	US6	
76	USB	1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNAS
68	IND8	
00	INDS	1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVREGNfSsCWVALTPTLAARNAS
67	IND5	1 YEVRNYSGYYHYTNDCSNSSIVYEAADMIMHTDGGARGARGARGARGARGARGARGARGARGARGARGARGAR
0,	INDS	1 IBVRNVSGVIHVTNDCSNSSIVYEAADMIMHTPGCVPCVREGNSSRCWVALTPTLAARNAS
73	SW2	1 YEVRNYSGYYHYINDCSNSSIVYETADMIMUTDCGUDGUDDAYASAGAAAA
, ,	342	1 IEVRIVSGVIHVINDCSNSSIVYETADMIMHTPGCVPCVREANSSRCWVALTPTLAARNES
63	нкз	1 YEVRNVSGIYHVTNDCSNSSylvethDMIMUTDCGUDGUDGUDGUDGU
	••••	1 18 VANVSGI IN VINDESNSSVVIETADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNVS
66	HK8	1 YEVRNVSGIYHVTNDCSNSSIVVETADMIMUTDGC-DGCDDDDDAGA
	••••	1 12 VRIV3GITRVINDCSNSSIVIETADMIMHTPGCmPCVRENNSSRCWVALTPTLAARNVS
61	D3	1 YEVRNVSGVYQVTNDCSNSSIVYETADMIMHTPGCVPCVREdNSSPCWVALTETLAADNAS
		IEVRNVSGVIQVINDCSNSSIVYETADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNSS
74	<b>T</b> 3	1 YEVRNYSGYYYUTNDCSNSSIVETADMIMUTDGGUDGDE AVGREEN AND AND AND AND AND AND AND AND AND AN
65	HK5	1 YEVRNVSGVYHVTNDCSN1SIVYETtDMIMHTDGCVDCXDENNSGCVXHIJ DDV
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVYEAVDVI HTTPGCVPCVPFNNSGEVALI TDDT N DNGG
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
69	P10	1 YEVRNVSGVYHVTNDCSNSSIVYEAADMIMHTPGCVPCVRENNSSRCWVALTPTLAARNSS
60	D1	1 YEVRNVSGVYHVTNDCSNSSIVYELADMIMHTPGCVPCVREdNSSRCWVALTPTLAARNgn
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVYEAADvIMHTPGCVPCVqEgNSSqCWVALTPTLAARNat
60.76		
60-76	consensus	yEVrNVSGvYhVTNDCSNsSiVyEaaDmImHTPGCvPCVrEnNsSrCWVALtPTLAARNas

### PIGURE 2B

SEO ID NO:	<u> Isolate</u>		
75	T10	62	VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHET1QDCNCSIYPGH1
62	DK1	. 62	IPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETaQDCNCSIYPGHV
64	HK4		
04	пл4	62	IPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
76	US6	62	VPTTTIRRHVDLLVGAAt FCSAMVVGDI CGSVEL i SOI ETES DE CHEMICO CONCERNO
•		~~	VPTTTIRRHVDLLVGAAtFCSAMYVGDLCGSVFLiSQLFTFSPRqHETVQDCNCSIYPGHV
68	IND8	62	VPTTTIRRHVDLLVGAAAFCSAMVVGDLCSVFLVSOLFTES PRODUCTION
67	IND5	62	VsTTTIRhHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
73	2		
73	SW2	62	VPTTTIRRHVDLLVGAAAFCSvMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
63	нкз	62	VPTETT PREVIOUS NOT A DECOMPOSE OF STATE OF STAT
		02	VPITITIRRIVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCS1YPGHV
66	HK8	62	VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVELVSOLETESBBBUETEVDDCNGSTVDGITE
2.			
61	D3	62	VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQeCNCSIYPGHV
74	тз		
/ 2	13	62	VPTKTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
65	HK5	62	VPTTaIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSOLFTFSPRRHETVODCNCSIVDGHU
			VPITATRRAVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRHETVQDCNCSIYPGHV
71	S45	62	VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSOLFTFSPRRHETVODCNCSTVDGHV
			[[]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]]
72	SA10	62	VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPRRYETVQDCNCSIYPGrV
69	P10		
O J	P10	62	VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSV1LVSQLFTFSPRRHWTVQDCNCSIYPGHV
60	D1	62 '	VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSVFLISOLFT]SPRRHETVOCCNCSIVPCUV
			VPITATRRHVDLLVGAAAFCSAMYVGDLCGSVFLISQLFT1SPRRHETVQeCNCSIYPGHV
70	S9	62 1	VPTTtIRRHVDLLVGAAvFCSAMYVGDLCGSVFLISQLFTiSPRRHETVQnCNCSIYPGHV
60.76			
60-76	consensus	•	VPTttIRrHVDLLVGAAaFCSaMYVGDLCGSVfLvSOLFTfSPRrheTvOdCNCs; vpch.

### FIGURE 2B

SEO ID NO	<u>): Isolate</u>		
75	T10	123	SGHRMAWDMMMNWSPTTALVvSQLLRIPQAVmDMVtGAHWGVLAGLAYYSMAGNWAKVLI
62	DK1	123	SGHRMAWDMMNWSPTTALVISQLLRIPQAVvDMVAGAHWGVLAGLAYYSMAGNWAKVLIT
64	HK4	123	SGHRMAWDMMNWSPTAALVVSQLLR1PQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
76	US6	123	SGHRMAWDMMNNWSPTAALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
•			
68	IND8	123	SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLI
67	IND5	123	SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLIV
73	SW2	123	SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIT
63	HK3	123	SGHRMAWDMMMNWSPTAALVVSOLLRIPOAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
66	HK8	123	SGHRMAWDMMMNWSPTLALVVSQLLRIPQAIVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
61	D3	123	TGHRMAWDMMNWSPTaalvvSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIT
74	<b>T</b> 3	123	TGHRMAWDMMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
65	HK5	123	TGHRMAWDMMNWSPTTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
71	S45	123	TGHRMAWDMMNWSPTaALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
72	SA10	123	TGHRMAWDMMNWSPTtalvvsQllripQaivDMvaGahwGvLaGLaYYSMvGNWAKVLiv
69	P10	123	sghrmawdmmnwsptaalvysgliripgaildvyagahwgylagiayysmygnwakyli;
60	D1	123	TGHRMAWDMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLIV
			<u> </u>
70	S9	123	TGHRMAWDMMNWSPTTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
60.76			
60-76	consensus		${\tt sGHRMAWDMMMNWSPTaALVvSQLLRiPQAvvDmVaGAHWGvLaGLAYYSMvGNWAKVLIV}$

# FIGURE 2B

SEO ID NO:	<u>Isolate</u>	104
75	T10	184 mLLFAGVDG
62	DK1	184 lLLFAGVDG
64	HK4	184 mLLFAGVDG
76	US6	184 lLLFAGVDG
68	IND8	184 MLLFAGVDG
67	IND5	184 MLLFAGVDG
73	SW2	184 MLLFAGVDG
63	нкз	 184 MLLFAGVDG
66	нк8	184 MLLFAGVDG
61	D3	 184 MLLFAGVDG
74	Т3	 184   LLFAGVDG
65	нк5	 184 MLLFAGVDG
71	S45	 184 MLLFAGVDG
72	SA10	 184 MLLFAGVDG
69	P10	184 MLLFAGVDG
60	Dl	 184 MLLFAGVDG
70	S9	184 MLLFAGVDG
60-76	consensus	mLLFAGVDG

### FIGURE 2C

SEO ID NO:	<u>Isolate</u> T2	,	A OVENTO TO VALUE OF THE OWNER OWNER OF THE OWNER OW
			AQV:NTs:gYMVTNDCSNeSITWQLQAAVLHVPGC:pCE:lGnTsrcwipvtpnvAvrQpG
78	T4	1	AQVKNTtnSYMVTNDCSNDSITWOLOAAVLHVPGCVPCEktGNTSRCWIPVSPNVAVRQPG
79	T9	1	AeVKNTSTSYMVTNDCSNDSITWOLQAAVLHVPGCVPCErVGNaSRCWIPVSPNVAVQRPG
80	US10	1	VQVKNTSTSYMVTNDCSNDSITWQLeAAVLHVPGCVPCEKVGNtSRCWIPVSPNVAVQRPG
77-80	consensus		aqVkNTstsYMVTNDCSNdSITWQLqAAVLHVPGCvPCE-vGNtSRCWIPVsPNVAVPG
SEQ ID NO:	<u>Isolate</u>		
77	T2	62	ALTOGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPrrHWFVQeCNCSIYPGTI
78	T4	62	ALTOGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFIVSPQHHWFVQdCNCSIYPGTI
79	Т9	62	ALTOGLRTHIDMVVMSATLCSALYVGDLCGGVMLAAQMFLiSPQHHWFVQECNCSIYPGTI
80	US10	62	ALTQGLRTHIDMVVMSATLCSALYVGDfCGGmMLAAQMFIvSPrHHsFVQECNCSIYPGTI
77-80	consensus		ALTQGLRTHIDMVVMSATLCSALYVGDlCGGvMLAAQMFlvSP-hHwFVQeCNCSIYPGTI
SEO ID NO:	<u>Isolate</u>		
77	<b>T</b> 2	123	TGHRMAWDMMNWSPTATMILAYAMRVPEVIiDIigGAHWGVMFGLAYFSMQGAWAKViVI
78	T4		TGHRMAWDMMMNWSPTATMILAYAMRVPEVIlDIvSGAHWGVMFGLAYFSMQGAWAKVVVI
79	Т9	123	TGHRMAWDMMMNWSPTtTMILAYAMRVPEVIIDIISGAHWGVMFGLAYFSMQGAWAKVVVI
80	US10	123	TGHRMAWDMMNWSPTaTlILAYvMRVPEVIIDIISGAHWGVlFGLAYFSMQGAWAKVVVI
77-80	consensus		TGHRMAWDMMMNWSPTaTmILAYaMRVPEVIiDIisGAHWGVmFGLAYFSMQGAWAKVvVI
SEO ID NO:	Toologe		
77	<u>Isolate</u> T2	184	LLLAAGVDA
78	<b>T4</b>	184	 LLLAAGVDA
79	Т9	184	III      LLLLAGVDA
80	US10	184	LLLaAGVDA
77-80	consensus	:	LLLaagvda

#### FIGURE 2D

82 83 84 81	D: Isolate DK11 SW3 T8 DK8 Consensus	1 VEVRNtSSSYYATNDCSNnSITWQLTNAVLHLPGCVPCENDNGTLHCWIQVTPNVAVKHRG
82 83 84 81 81-84	DE D	62 ALTHNLRAHIDMIVMAATVCSALYVGDVCGAVMIVSQAFIVSPEHHHFTQECNCSIYQGHI
SEQ ID NO 82 83 84 81	E Isolate DK11 SW3 T8 DK8 Consensus	123 TGHRMAWDMMLNWSPTLTMILAYAARVPELVLEVVFGGHWGVVFGLAYFSMQGAWAKVIAI
SEO ID NO 82 83 84 81	Isolate DK11 SW3 T8 DK8 Consensus	184 LLLVAGVDA          184 LLLVAGVDA          184 LLLVAGVDA          184 LLLVAGVDA LLLVAGVDA

#### FIGURE 2E

SEO ID NO:	: <u>Isolate</u> DK12	1 I EWDNIGGI WIT TATOG NGGELIGON DOLLAR DE CONTROL DE C
87	•	1 LEWRNVSGLYVLTNDCsNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSVTPTVAVRYVG
	HK10	LEWRNVSGLYVLINDCPNSSIVYEADDVILHTPGCVPCVQDGNTSTCWTSVTPTVAVRYVG
88	· S2	1 LEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVODGNTSTCWTPVTPTVAVRYVG
90	S54	1 LEWRITSGLY:LINDCSNSSIVYEADDVILHTPGCVPCVODGNTSTCWTPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
89	S52	1 LEWRNTSGLYVLTNDCSNSSIVYEADDVILHTPGCVPCVQDGNTSmCWTPVTPTVAVRYVG
86-90	consensus	LEWRNtSGLYvLTNDCsNSSIVYEADDVILHTPGCVPCVQDGNTStCWTpVTPTVAVRYVG
SEO ID NO:	Isolate	
86	DK12	62 ATTASIRSHVDLLVGAATMCSALYVGDvCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
87	HK10	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFPPPPPHQTVQTQNCSIVPCVI
88	S2	62 ATTASIRSHVDLLVGAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
90	S54	62 ATTASIRSHVDLLVGAATICSALYVGDMCGAVELVGAATTERPREDUCTION
89	<b>S52</b>	
86-90	consensus	ATTASIRSHVDLLVGAATmCSALYVGDmCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGH1
		- Z
SEO ID NO:	<u>Isolate</u> DK12	123 SGHRMAWDMMNWSPAVGMVVAHVLRLPQTLFDIIAGAHWGIMAGLAYYSMQGNWAKVAII
87	HK10	
88	S2	123 SGHRMAWDMMMWSPAVGMVVAHVLRLPOTLFDIIAGAHWGILAGLAYYSMOGNWAKVAII
V		SGRRMAWDMMNWSPAVGMVVAHVLRLPOTVFDIIAGAHWGILAGLAYYSMOGNWAKVAII
90	S54	123 SGHRMAWDMMNWSPAVGMVVAHILRLPOTLFDILAGAHWGILAGLAYYSMOGNWAKVAII
89	S52	123 SGHRMAWDMMNWSPAVGMVVAHILRLPQTLFDILAGAHWGILAGLAYYSMQGNWAKVAIV
86-90	consensus	SGHRMAWDMMMNWSPAVGMVVAHvLRLPQT1FDIiAGAHWGIlAGLAYYSMQGNWAKVAIi
SEO ID NO:	Isolate	
86	DK12	184 MVMFSGVDA
87	HK10	 184 MYMFSGVDA
88	S2	 184 MVMFSGVDA
90	S54	
89	S52	 184 MIMFSGVDA
		1

86-90

consensus

MvMFSGVDA

## FIGURE 2F

SEO ID NO:       Isolate         94       27         93       Z6         93-94 consensus (Z6)	1 VNYhNASGVYHITNDCPNSSImYEAEHHILHLPGCVPCVReGNQSRCWVALTPTVAAPYIG
SEO ID NO:         Isolate           94         Z7           93         Z6           93-94 consensus (Z6)	62 APLESIRRHVDLMVGAATVCSALYIGDLCGGVFLVGQMFSFQPRRHWITQDCNCSIYAGHV
SEO ID NO:       Isolate         94       Z7         93       Z6         93-94 consensus (Z6)	123 TGHRMAWDMMNWSPTTTLvLaQvMRiPSTLvDLLTGGHWGiLiGvAYFcMQANWAKVILV
SEO ID NO:         Isolate           94         Z7           93         Z6           93-94 consensus (Z6)	184 LFLYAGVDA          184 LFLFAGVDA LFLFAGVDA

#### FIGURE 2G

SEO ID NO			
36	SA5	<pre>1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVkegNVSRCWVQITPTL;</pre>	SAPNLG
100	SA7	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQnNVSRCWVQITPTL	SAPNLG
97	SA4	1 VPYRNASGVYHVTNDCPNSSIVYEADNLILHAPGCVPCVRQDNVSkCWVQITPTL	 SAPNLG
96	SA1	1 VPYRNASGVYHVINDCPNSSIVYEADsLILHAPGCVPCVRQDNVSRCWVQITPTL:	 SAPtfG
99	SA6	1 VPYRNASGVYHVINDCPNSSIVYEADDLILHAPGCVPCVRkDNVSRCWVhITPTL	H = H
101	SA13	1 VPYRNASGVYHVTNDCPNSSIVYEADDLILHAPGCVPCVRqgNVSRCWVqITPTLS	
96-101	consensus	VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVPCVrqdNVSrCWVqITPTLS	
SEO ID NO:	<u>Isolate</u>		
98	SA5	62 AVTAPLRRVVDYLAGGAALCSALYVGDACGAVFLVGQMFtYRPRQHTTVQDCNCSI	IYSGHI
100	SA7	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFsYRPRQHTIVODCNCS	 [YSGHI
97	SA4	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFTYRPRQHTTVQDCNCSI	  YSGHI
96	SA1	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFTYRPRQHTIVQDCNCSI	
99	SA6	62 AVTAPLRRAVDYLAGGAALCSALYVGDvCGAlFLVGQMFTYRPRQHaTVQDCNCSI	
101	SA13		YSGHI
96-101	consensus	AVTAPLRRaVDYLAGGAALCSALYVGDaCGAvFLVGQMFtYrPRqHttVQDCNCSI	
SEO ID NO.	T==1===		
SEO ID NO: 98	<u>Isolate</u> SA5	123 TGHRMAWDMMMNWSPTTALVMAQvLRIPQVVIDIIAGGHWGVLFAVAYFASAANWA	KVVT.V
100	SA7	123 TGHRMAWDMMMNWSPTTALIMAOLI BIROLUTTATA COLUMNIA	KVVLV
97	SA4	123 TGHRMAWDMMNWSPTTALLMAQLLRIPQVVIDIIAGGHWGVLFAAAYFASAANWA	11 11
96	SA1	123 TGHRMAWDMTTNWSPTTALLMAQMLRIPQVVIDIIAGGHWGVLFAAAYFASAANWA	
99	SA6	123 TGHRMAWDMMNWSPaTALVMAQMLRIPQVVIDIIAGGHWGVLFAAAYFASAANWA	
101	SA13		KAA19
96-101	consensus	TGHRMAWDMMMNWSPtTALvMAQlLRIPQVVIDIIAGgHWGVLFA&AYfASAANWA	

#### FIGURE 2G

SEO ID NO:	<u>lsolate</u>		
98	SA5	184	LFLFAGVDg
100	SA7	184	LFLFAGVDA
			11111111
97	· SA4	184	LFLFAGVDA
96	03.1		1111111
96	SA1	184	LFLFAGVDg
99	SA6	104	
,,	SAG	184	LFLFAGVDA
101	SA13	184	LFLFAGVDA
	0	201	DIBINGVDA
96-101	consensus		LFLFAGVDa

# FIGURE 2H

SEO ID	NO: Genotype																		
81-84	(IV/2b)		l VEVRNi	Sesy	YATN	DCSN	nST	רשים	T.Tw	דנות	ut n	con	MOEN		·				
85	(2c)	3	L VEVKDI	GDSY	MPTN	DCSN	CCI	. TMO	TEC	IMV L	THE P	GC V	PCEN	DNGI	TICA	IQV	TPNV	AVI	CHRC
77-80	(III/2a)	]	agvkNi	stsY	MVTN	DCSN	725	TWO	T.~N	MANT.	n i Pi	GC V	PCER	TANV	SRCW	VPV	APNL	AIS	SQPC
86-90	(V/3a)	1	LEWRNE	SGLY	VLTN	DCeN	SSI	מאנו.	שמעע	NAV L		GCV	PCEK	VGNE	SKCW	TBA	SPNV	AVC	<b>Id</b> bc
60-76	(II/1b)	1	YEVENV	SGvY	hVTN	DCSN	-Ci	17:E	220	- T-1		GC V	PCVQ	DGNT	SECW	īδΛ	TPTV.	AVI	<b>SYV</b> €
52-59	(I/la)	j	YOURNS	tGLY	HVTN	DCPN	SST	AAR	a A D	TT 1	n a Pa	CCV	PCVI	FUNE	STCW	VAL	tPTL	AAF	≀Na :
91	(4a)	]	EHYRNA	SGIY	HITN	DCPN	55T	. VVE	מתע	CITT	nsp(	CCV	PCVK	Egna	SICW	vav	tPTV.	ATF	<b>WGK</b>
93-94	(4c)	j	VNYTNA	SGVY	HVTN	DCPN	SST	vVE	YEN Ven	~TT1	DEPO	3C V	PCVM	IGNI	SRCW	LbA	TPTV.	AVA	HPC
95	(4d)	ī	YNYRNS	SGVY	HVTN	DCDN	33 I	17VE	TOV	UTTI	DI D	3C.T	PCVK	VGNQ	SRCW	VAL	TPTV.	Ave	YIC
92	(4b)	ī	VHYRNA	SGVY	HVTN	DCPN	TOT	(IVE	TOI	TITM	יש אנו אלו דנו	300	PCVK	EGNK	STCW	VSL	TPTV.	AAÇ	OHTV
96-101	(5a)	1	VPYRNA	SGVY	HVTN	CPN	SST	WE	<i>y D</i> ~	1 TT 1	ロカカノ	3C V.	PCVR	TEMI.	SRCW	VPL	TPTV.	AAF	Abv
102	(6a)	ī	LTYGNS	SGLY	תרינו	חרפאי	33 I	A TE	WD Y.	MTT I	TAP	3C V	PCVE	dann	SICW	vqI	TPTL:	SAF	nlG
						J C 1 11.	JJ 1	A TIES	HUM	MIT IN	TLP	ىداد	PCVR	VDDR	STCW	HAV	TPTL	AIF	NAS
52-102	consensus			Y	TNI	DC N	S				H PC	~~	D.C		~		_		
				-			5				י אר	<b>3</b> C .	PC		CW		P		
SEO ID	NO: Genotype																		
81-84	(IV/2b)	62	ALTHNL	RtHvi	Om T VA	דד מ מי	700	ል ተ. ህፕ	ZCD.		17747		2257						
85	(2c)	62	ALTKGL	RAHII	DITU	TARK	700	AT.VI	יתבטי	vcar	7 A E-17	. N.N.	SWIT:	ISPE	CHDF"	COE	INCS:	LYQ	GhI
77-80	(III/2a)	62	ALTOGL	RTHI	OMVVN	1SATT		ΔΙ.V1	MCD.	v CGr	`N/7	- 2 2 4		A S P OI	HTF	/QE	INCS.	ΙΥΡ	GRI
86-90	(V/3a)	62	ATTASI	RSHVI	OT.T.VC	ידעענ	nCS	ALLI At.Vi	MGD.	-CC2	ALTE	-12-C	SMF.T.	VSPQ	1HWF	/Qe	INCS	ΙΥΡ	GTI
60-76	(II/1b)	62	VpTttI	RrHVI	DITIVO	LAASI	700	nui (	וחבע		17 <i>7</i> 27	·^G(	SVE LAIN	RPRI	SHOL	/QT	CNCSI	JYP	GHl
52-59	(I/1a)	62	LPatQL	RRhTI	OT.T.VC	SATI		77.TA	ים נעטי		ATT	172/	)	SPRI	rneil	ZQQ(	CNCS	YP	Ghv
91	(4a)	62	APLESF	RRHVI	LMVC	ידע מבי		י בעבר דע.זא	ומטי		, y L. t	vg	777 L.I.I	SPR	rnw11	'Qa	CNCS	ΙΥΡ	GHI
93-94	(4c)	62	APLESI	RRHVI	TIMUC	דרממי	1001	7T V+	יםם. נעם		MAP L	TIC.	SWT.L.	RPRI	SHMIL	QE	CNCS	YT	GHI
95	(4d)	62	APLESLI	RRHVI	LMVC	CATT	.00	NUL V	נתטי		ar L	νGζ γος	SWE 21	OPRI	CHW11	ODO	INCS	YA	GHi
92	(4b)	62	APLESM	RRHVI	IMVC	DATE	4C S 2	VEA1	CDI		1 V E L	100¢	ST LINE	OPRI	CHWII	ODC	INCS	YT	GHI
96-101	(5a)	62	AVTAPLI	RRAVI	YI.AC	TAAD	.00	AT.VI	MD:			10GC	STRUE	KPK	CHWIT	QDO	INCS 1	ΥP	GHV
102	(6a)	62	TPATGF	RHVI	DALLIC	DAVE	700	ST.VI	CDI		TET	20V	ALTE CI	TPRO	THEEN	QDC	NCSI	YS	GHI
								,,,,	. GDI	ucus	LLL	MO.	STL IF	. ÖbKi	GHM.I.A	QDC	NCSI	YT	GHV
52-102	consensus		I	R I	)	A	CS	v	GD	CG		_		_					_
			_	_		••		•	GD	CG		Ç	į	₽		Q	NCS	Y	G
SEO ID	NO: Genotype																		
81-84	(IV/2b)	123	TGHRMAN	DMMI.	NWSP	TLTM	TT.Z	ממענ	DVE	PT.37	T.A.T	TEC	CUNC	'' II II C		~~~			
85	(2c)	123	TGHRMAN	/DMMM	NWSP	TTTM	T.T.Z	VT.V	DIE	FUT	TUT	V F G	CUMC	700EC	LAYE	SMC	KGAWA	KV.	IAI
77-80	(III/2a)	123	TGHRMAN	DMMM	NWSP	TaTm	TTZ	YaM	Dir	TVE	int	100	'A LIWC	ALTE C	LAXE	SMC	GSWA	KV.	IVI
86-90	(V/3a)		COUNTY	I D LITTAL	MM25	AVGM	VVE	MVI.	. W T . E	וידראי	TOTE	inc	י אנדעות	T 7 7 7	T BREEF	-	~~~		
60-76	(II/1b)	123	BGHRMAW	DMMM	NWSP	TaAL	Vvs	OLL	Dip	ΩΔ32 ΩΔ32	rDT.	TAG	A LIMO	LIAG	TAXX	SMQ	GNWA	KV2	Ali
52-59	(I/1a)	123	TGHRMAW	DMMM	NWSP	Trat.	Vva	OT.T.	Dip	O24	TDM	V A G	BULLO	VIIAG	LAYY	SMV	GNWA	KVI	LIV
91	(4a)	123	TGHRMAW	DMMM	NWSP	LLLI.	T.T.2	OTM	D1/10	TAT.	בייונון ביייייייייייייייייייייייייייייייייייי	ひとし	CUMC	VLAG	LAYF	SMV	GNWA	KV.	LvV
93-94	(4c)	123	TGHRMAW	DMMM	NWSP	Lalalı. 1	מ.ד ו	(U) VW	AVE DID	CTT.		ひんり	CURRO	V LAG	LAYF.	SMQ	GNWA	ΚV	ΛLV
95	(4d)	123	TGHRMAW	DMMM	NWSP	TATT	VT.D	OLM	DID	CYM	ADT.	ו אר	CULIC	VLVG	LAYF.	smQ	AWWA	KV]	LLV
92	(4b)	123	SGHRMAW	DMMM	NWSP	TSAT.	TMA	OTT	DID	CTT	CDI.	unii Tav	CURIC	TTAC	LAYF	SMQ	AWWA	KV]	LLV
96-101	(5a)	423	TOURGIVE		MM25	L.I.WI	чма	mır.	סדס	אאר	TDT	TNへ	~~~	277 772					
102	(6a)	123	TGHRMAW	DMMM	NWSP'	TTTI:	VT.S	STI	DIND	RIC:	TUI.	エアク	GIRAG	VLFA	aayf)	ASA	AWWA	K۷٦	LV
							<i></i>	11.			. ۷ <i>حب</i>	4 F G	OUMG	ALLLA	VAYF(	JMA	GNWL	KVI	AV.
52-102	consenus		GHRMAW	DMM I	NWSP			,	R P			~	HWG						
								•				G	пWG		A		W	ΚV	

## FIGURE 2H

SEO ID NO	<u>): Genotype</u>		
81-84	(IV/2b)	184	LLLVAGVDA
85	(2c)	184	LLLTAGVEA
77-80	(III/2a)	184	LLLaAGVDA
86-90	(V/3a)	184	MvMFSGVDA
60-76	(II/1b)	184	mLLFAGVDG
52-59	(I/la)	184	LLLFaGVDA
91	(4a)	184	LFLFAGVDA
93-94	(4c)	184	LFLfAGVDA
95	(4d)	184	LFLFAGVDA
92	(4b)	184	LFLFAGVEG
96-101	(5a)	184	LFLFAGVDa
102	(6a)	184	LFLFAGVEA
52-102	consensus		GV

# PIGURE 3

) jsv£lv	-AVMIV -AVMIV -AVMIV	AVELA	GOVMILA	AVELV AVETV	SVFLV	SVFLV SVFLV	SVFLV	SVFLV SVFLV	SVFLV	-SVFLY -SVFL1	-SV1LV -SVFLV	SVFLV SVFLV SVFLI	SVFLI	S	SVEEV	SVFIV	GAF	GAFLV	GVFLV	יייייייייייייייייייייייייייייייייייייי	AVFLV	AVFLV	AIFLV	BlFLa
0 	- N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N N - N N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N - N -	AL- V V	AL-V-f-	MI-VM	W-V-L-	Z-0L					-7X-W		L-V-L-		E-VL	L-VL	AL-VL	AL-V-L-	-AL-IL	)f T - ]	L-V-A	- A		L-11
270 270 vgaAt1ČSe	222	<u> </u>	N S S S S S S S S S S S S S S S S S S S	LLVGA-TM7 LLVGA-TM7 LLVGA-TM7 LLVGA-TL7	14	LVGA-AF	LVGA-AF	44	ממי	LLVGA-AF	LVGA-AFP	44>	<b>イ</b> トウェ	768-TL7	/GS-TLA	/GS-TL/		<b>TV</b> :	Ž E	T.		YLAGG-ALA	YLAGG-AL-A	1 LAGa - vv 9
260 LRrhvDllv	L-AHi-MIVMA L-AHV-MIVMA L-THV-VIVMA	AHT.		22222	17	- DHV - I	- 25. - 25. - 1		74,	I - RHV - LLV I - RHV - LLV		I - RHV - LLV I - RHV - LLV I - RHV - LLV	E E		至至	L-RHI-LLV L-RYI-LLV L-PHI-LLV	E - RHV - LMVGA -	١.			PAC V	RA S	22	RhV-
250 260 27 tvaarnagaptttlRrhvDllvgaAtl	NVAVKHRGALTHNL-AHİ NVAVKHRGALTHNL-AHV NVAVKHRGALTHNL-THV NVAVKHPGAİ TÜNL	N A SANTAGALIAND	S-NVAVrOPGALITGGL-TE S-NVAVQRPGALITGGL-TE S-NVAVQRPGALITGGL-TE NVAVQRPGALITGGL-TE	TVAVRYVGATTAS TVAVRYVGATTAS TVAVRYVGATTAS TVAVRYVGATTAS	TLAARNASVOTTT	TLAARNASVBITT TLAARNESVPTTT	TLAARNVSVPTTT TLAARNVSVPTTT	ILAAKNSSVPI-IT TLAARNSSVPTTT	200	TLAAKNASIPITT TLAARNASVPITT	- TLAARNSSVPTTA	TLAARNASIPTT TLAARNAEVPTTT	TVATRDGKLPTaQL-	IVATEDGELPTTOL-	I VATROGKLPATOI TVATROGKLPATOI	IVATROGKLPATOL- IVATROGKLPATOL- IVATROGKLPATOL-	tPVT-TVAVahpGAPLeSf	VALT-TVAVBYIGAPLdS1	TVAADY IGAPLES	TVAAPvnNAPI.ESm	TLSAPNIGAVTAPL-	FLSAPNIGAVTAPL	TLSAPSLGAVTAPI TLSAPSLGAVTAPI	-TLaiPnastpatgf-
240 * ErCWavtP		v pva	VIII	TSVT- TSVT- TPVT-	VALT	NALT-	VAL:	VALT	- VALA	- N	-VALT	VALT	VAMT	- VAVI	- VAVI	VAVA-	:	:	VALT	-VnI.T	-VOIT	VOIT-	VAIT-1	havT
230 * vPCvregnt	-V ENDNGTLH -V ENDNGTLH -V ENDNGTLR	ErTa	V EKTGNTSR V EKVGNTSR V ERVGNASR	-V-VODGNTST -V-VODGNTST -V-VODGNTST -V-VODGNTST -V-VODGNTST	-V - VREGNESB	- V - VREANSSR - V - VREANSSR	-VVRENNSSR -MVRENNSSR	-VVREGNSSR -VVREGNSSR	-VVRBBNSSR -VVRENNSSR VVRENNSSR	-VVKENNSSK -VVRENNSSK	-VVRENNSSR -VVRENNSSR	-VVREDNSSK -VVREDNSSG -VVGEGNSSG	-VVREGNVSR	-VVREGNESR -VVREGNESR	-VVREGNASK -VVREGNASK	- V VREGGADOK - V VREGNESR - V VREGNESR	-VVmtGNtSR	-1VRVGNQSR	V VEGNOSE		V VkegNVSR	V - VRODNVSK	V VRKDNVSR	.lVRvddrSt
10 220 <u>S</u> ivyeaadallHtPGC	CWOLTNAVL-L CWOLTNAVL-L CWOLTDAVL-L CWOLTDAVL-L	vWOLegAVL-t	TWOLGAAVL-V TWOLGAAVL-V TWOLOAAVL-V	VYEADDVIL-T VYEADDVIL-T VYEADDVIL-T VYEADDVIL-T VYEADDVIL-T	VYEAADMIM-T	YETADMIM-T-	VIETADMIM-T-	VYETADMIM-T-	VYETCOMIM-T-	VYEAADMIM-T-	YEAADMIM-T	VYEAVDVIM-T-	YEAADAIL-T	YEANDAIL-T-	YEAADAIL-S-	VYETADALL-S VYETADALL-a VYETADELL-a	VYEACHHIL-L-	VYEAEHQIL-L	MYEAEHHIL-L-	VYETEPHIM-1	VYEADNLIL-A	VYEADNLIL-A-	YEADDLIL-A	V1EADamIL-1
CBNB	CI - CI - CI - CI - CI - CI - CI - CI -	S-8-I	0.00.00 0.00.00	N. N. N. N. N. N. N. N. N. N. N. N. N. N	I-8-8	1-S-S-					သလင်		0.0			2.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	P-S-I	I-S-	P-S-Im	P-t-I	S.	S. S.	P-S-IV	ij.
200 yevr <u>nva</u> gvyhvTND	VEVRNESS-YA- VEVRNISSS-YA- VEVRNISSS-YA- VEVRNTSES-YA-		AOVKNTSTS-MV- VOVKNTSTS-MV- AEVKNTSTS-MV- AQVRNTSFG-MV-	LEWRNVSGL-VL- LEWRNVSGL-VL- LEWRNTSGL-VL- LEWRNTSGL-1L- LEWRNTSGL-1L-	YEVRNVSGV-HV-	YEVRINGGY-HV-	YEVRNVSGI - HV - YEVRNVSGI - HV -	YEVRNVSGV-QV-	YEVRIVSGV-YV-	YEVRNVSGM-HV-	YEVRNVSGW-HV-	YEVRNVSGA-HV- YEVRNVSGA-HV- VEVDNVSGA-HV-	YOVRNSTGL-HV-	HOVRNSTGL-HV-	YOVENSSGL-HV-	YOVRNSTGL-HV- YOVRNSTGL-HV-	•hYRNASGi-Hi-	VNYRNASGV-Hv-	VNYPNASGV-H1-	봄	VPYRNASGV-HV- VPYRNASGV-HV-	VPYRNASGV-HV-	VPYRNASGV-HV-	ltYgN8SG1-H1-
Isolate	DK11 SW3 DK8 T8	583	T4 US10 T9 T2	DK12 HK10 S2 S54 S52	IND8	SW2	HY W W W W	ב המני המני	HKS HK4	0.56	SAIO	S9 S9 S9 S9	DK7	024	1625	S14 14 18	24	92	27 DK13	Z1	SAS SA7	SA1	SA6 SA13	HK2
SEQ ID NO: 52-102	8888 2214 44		78 80 77 77	8890899	89	· m r	n <b>w</b> –	1.11	r W 4	*100	V 63 IA	nnoc	200	ງເບດ /ເບ 4	rm o	0.0.0 0.0.0	91	93	44			60 70 70	99 101	102
Genotype	IV/2b	2c	111/2a	(V)/3a					11/11					•	1/1a		48	4°C	4	4 b		<b>5</b> a		ę 9

# FIGURE 3

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FIGURE 4

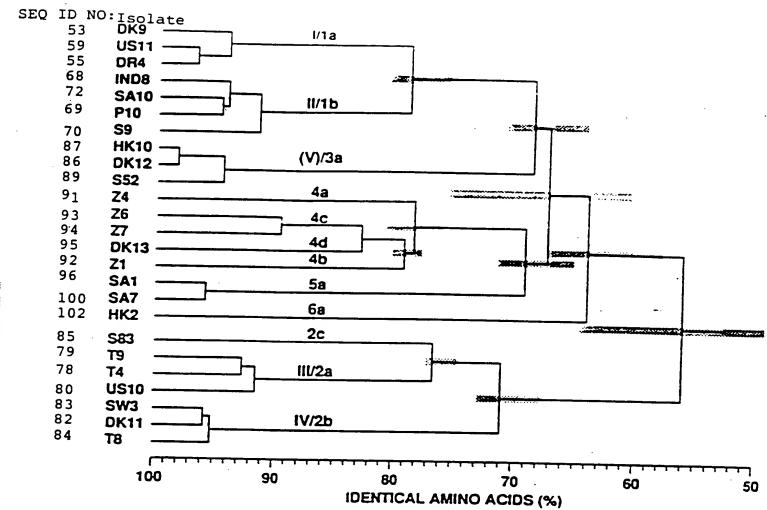
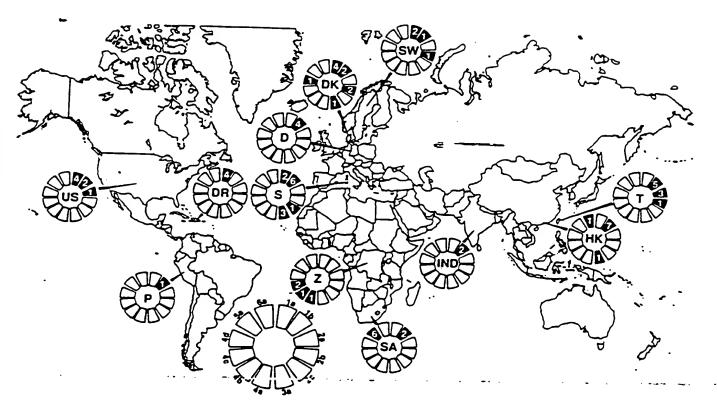


FIGURE 5



#### FIGURE 6A

SEQ ID NO: ISOLATE 108 DR4 103 DK7 104 US11 105 S14 106 SW1 107 S18	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
103-108 consensus	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
SEQ ID NO:         ISOLATE           108         DR4           103         DK7           104         US11           105         S14           106         SW1           107         S18	62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG 63 ACGTLAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
103-108 consensus	ACGTcAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
SEO ID NO:         ISOLATE           108         DR4           103         DK7           104         US11           105         S14           106         SW1           107         S18	123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGA 123 CCCTAGATTGGGTGTGCGCGCGCGAGGAAGACTTCCGAGCGTCGCAACCTCGAGGTAGA 123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGTCGCAACCTCGAGGTAGA 123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGTCGCAACCTCGAGGTAGA 124 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGTCGCAACCTCGAGGTAGA 125 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGCGGTAGA
103-108 consensus	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGCGGTCGCAACCTCGAGGTAGA
SEQ ID NO:         ISOLATE           108         DR4           103         DK7           104         US11           105         S14           106         SW1           107         S18	184 CGTCAGCCTATCCCCAAGGCgCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC 184 CGTCAGCCTATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC 184 CGTCAGCCTATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC 184 CGTCAGCCTATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC 184 CGTCAGCCTATCCCCAAGGCGCGCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC 184 CGTCAGCCTATCCCCAAGGCGCGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103-108 consensus	CGTCAGCCTATCCCCAAGGC-CGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTAcC
SEO ID NO:         ISOLATE           108         DR4           103         DK7           104         US11           105         S14           106         SW1           107         S18	245 CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCcCCCGTGG 245 CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG 245 CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG 245 CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG 245 CTTGGCCCCTCTATGGCAATGAGGGCTGCGGATGGCGGGATGGCTCCTGTCCCCCGTGG 245 CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCCCCCCGTGG
103-108 consensus	CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTC-CCCCGTGG
SEO ID NO:         ISOLATE           108         DR4           103         DK7           104         US11           105         S14           106         SW1           107         S18           103-108         consensus	CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGLAGGTCGCGCAATTTGGGTAAGGTC CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGLAGGTCGCGCAATTTGGGTAAGGTC CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC CTCTCGGCCTAGCTGGGGCCCTACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC CTCCCGGCCTAGCTGGGGCCCTACAGACCCCCGGCGTAGGTCGCGCAATTTGGGCAAAGTC CTCCCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGCAAAGTC

103-108

consensus

# FIGURE 6A

SEO ID NO:	<b>ISOLATE</b>		
108	DR4	367	ATCGACACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATcCCGCTCGTCGGCGCCC
103	DK7	367	ATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
104	US11	367	ATCGATACCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
105	S14	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
106	SW1	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
107	S18	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
		•	
103-108	consensus		ATCGALACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATaCCGCTCGTCGGCGCCC
			·
SEO ID NO:	<u> ISOLATE</u>		
108	DR4	428	CcCTTGGgGGCGCTGCCAGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAGACGGCGTGAA
103	DK7	428	CTCTTGGAGGCGCTGCCAGGCCCTGGCGCATGCCGTCCGGGTTCTGGAAGACGCGTGAA
104	US11	428	CTCTCGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
105	S14	428	CCCTCGGGGGCGCTGCCAGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
106	SW1	428	CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
107	S18	428	CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
		_	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
103-108	consensus		CtCT-GGaGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
•			www.seeseeseeseeseeseeseeseeseeseeseeseesee
SEO ID NO:	ISOLATE		
108	DR4	489	CTATGCAACAGGGAALCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCLLTGCTCTCT
103	DK7	489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTTGGCCCTGCTCTCT
104	US11	489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTC
105	S14	489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTcCTaGCCCTGCTTTCT
106	SW1	489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTC
107	S18		CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTTCTTCTTCTTCTTCTGGCCCTGCTCTCT
	0.20	-05	CINICAL CONTROL
103-108	consensus		CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTtcTgGCccTGCTcTCT
_			· · · · · · · · · · · · · · · · · · ·
SEO ID NO:	<u>ISOLATE</u>		
108	DR4	550	TGCtTGACCGTGCCCGCaTCGGCC
103	DK7	550	TGCCTGACCGTGCCCGCTTCGGCC
104	US11	550	TGCCTGACTGTGCCCGCTTCAGCC
105	S14		TGCCTGACTGTGCCCGCTTCAGCC
106	SW1	550	TGCCTGACaGTGCCCGCGTCAGCC
107	S18		TGECTGACEGTGCCGCGTCAGCE

TGccTGACtGTGCCCGCtTCaGCc

SEO ID NO:	<b>ISOLATE</b>	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
118	IND8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
116 122	SW2 HK4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAGACCAAACGTAACACCAACCGCCGCCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGACAAACCAAACGTAACACCAACCGCCGCCCACAGG
123	P8	1 ATGAGCACGACTCCTAAACCTCAAAGACAAACCAAACGTAACACCGACCG
124	T3	1 ATGAGCACGAGTCCTAAACCTCAAAGAAAAACCAAACGTAACACCAGCCGCCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
121	HK5	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
	••••	
109-124 c	onsensus	ATGAGCACGAaTCCTAAACCTCAAAGAaAaACCAAACGTAACACCAaCCGCCGCCCACAGG
SEO ID NO:	ISOLATE	
3EO 1D NO:	S9	62 ACGTLAAGTTCCCGGGCGGTGGLCAGATCGTCGGTGGAGTTTACCTGTTGCCGCGCAGGGG
117	IND3	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
118	IND8	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
111	D1	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
112	US6	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
113	P10	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
114	DK1	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
115	T10	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
116	SW2	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
122	HK4	62 ACGTLAAGTTCCCGGGCGGTGGCCAGATCGTcGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109	SA10	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTCTAtCTGTTGCCGCGCAGGGG
110	S45	62 ACGTCAAGTTCCCGGGtGGCGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
123	P8	62 ACGTTAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
124	<b>T</b> 3	62 ACGTTAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
120	HK3	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
121	HK5	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
109-124 C	onsensus	ACGTCAAGTTCCCGGGCGGLGGLCAGATCGTLGGTGGAGTLTACCTGTTGCCGCGCAGGGG
SEO ID NO:	ISOLATE	
119	S9	123 CCCCAGGTTGGGTGTGCGCGC&ACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
117	IND3	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
118	IND8	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
111	D1	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
112	US6	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
113	P10	123 CCCCAGGTTGGGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
114	DK1	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
115	T10	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
116	SW2	123 CCCCcGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
122	HK4	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
109	SA10	123 CCCCAGGTTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
110	S45	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCaCAACCTCGTGGACGG
123	P8	123 CCCCAGGTTGGGTGTGCGCGACTAGGAAGACTTCCGAGCGaTCGCAACCTCGTGGCAGG
124	Т3	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
120	HK3	123 CCCCAGGTTGGGTGTGCGCGCGACCAGGAAGACTTCaGAGCGGTCGCAACCTCGTGGAAGG
121	HK5	123 CCCCAGGTTGGGTGTGCGCGCGACCAGGAAGACTTCcGAGCGGTCGCAACCTCGTGGAAGG
109-124 cc	nsensus	CCCCaGGTTGGGTGTGCGCGCgACtAGGAAGACTTCcGAGCGgTCgCAACCTCGTGGaaGG
CEO TE ***	****	
<u>SEO ID NO:</u> 119	<u>ISOLATE</u> S9	184 CGACAACCTATCCCCAAGGCTCGCCatCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC

	117	IND3	184	CGACAACCTATCCCCAAGGCTCGCCGGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGTACC
	118	IND8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGCACC
	111	D1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGTACC
	112	บริธ	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
	113	P10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
	114	DK1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
	115	T10	184	CGACAGCCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
	116	SW2	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCtGGGTACC
	122	HK4	184	CGACAACCTATCCCCAAGGCTCGCCAACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
	109	SA10	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGACCTGGGCCCAGCCCGGGTACC
	110	\$45	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCCCAGCCCGGGCAtC
	123	P8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGCACC
	124	T3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGTACC
	120	HK3	184	CGACAACCTATCCCCAAGGCTCGCCaACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
	121	HK5	184	CGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
				CONTROL PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
	109-124	consensus		$\tt CGACAaCCTATCCCCAAGGCTCGCCggCCCGAGGGCAGGgCCTGGGCCCGGGCACCCGGGCAGGGCA$
	SEO ID N	O: ISOLATE		
	119	S9	245	CTTGGCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGtGG
	117	IND3	245	CTTGGCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGEGG
7	118	IND8	245	CTTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
≓ =1:	111	D1	245	CTTGGCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
<u>.</u>	112	US6	245	CTTGGCCCCTCTATGGCAACGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
7	113	P10	245	CTTGGCCCCTCTATGGCAATGAGGGCtTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
j	114	DK1	245	CTTGGCCCCTCTATGGCAATGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGGGG
=	115	T10	245	CTTGGCCCCTCTATGGCAATGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGEGG
=	116	SW2	245	CCTGGCCCCTCTATGGCAATGAGGGCATGGGATGGCAGGATGGCTCCTGTCCCCCCGCGG
-	122	HK4	245	CTTGGCCCCTCTATGGCAATGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
1	109	SA10	245	CTTGGCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
£	110	\$45	245	CTTGGCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
	123	P8	245	CTTGGCCCCTCTATGcCAATGAGGGCTTGGGGTGGGCGGGATGGCTCCTGTCACCCCGCGG
5	124	Т3	245	CTTGGCCCCTCTATGGCGACGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
ž	120	HK3	245	CTTGGCCCCTCTATGGCAACGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
1	121	HK5	245	CTTGGCCCCTCTATGGCAALGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCaLGG
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i i	109-124	consensus		CtTGGCCCCTCTAtGgCaAtGAGGGC-TGGGgTGGGCaGGATGGCTCCTGTCaCCCCgcGG
1				
di F				
,	SEO ID NO	D: ISOLATE		
	119	S9	306	CTCTCGGCCTAGTTGGGGCCCCAatGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
	117	IND3	306	TTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAagtC
	118	IND8	306	CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
	111	D1	306	CTCCCGGCCTAGTTGGGGCCCCACcGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
	112	US6	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTCGGTAACGTC
	113	P10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGCGTAACGTC
	114	DK1	306	CTCTCGGCCTAGTTGGGGCCCCAacGACCCCCGGCGTAGGTCGCGTAATTTGGGTAACGTC
	115	T10	306	CTCcCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
	116	SW2	306	CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCGGCGTAGGTCGCGTAATTTGGGTAACGTC
	122	HK4	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAACGTC
	109	SA10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGtAATTTGGGTAAGGTC
	110	S45	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
	123	P8	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTCCGTAACGTC
	124	<b>T</b> 3	306	CTCCCGGCCTAATTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGtAATcTGGGTAAGGTC
	120	HK3	306	CTCTCGGCCTAATTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTTCGGTAACGTC
	121	HK5	306	CTCTCGGCCTAgTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGLAATTTGGGTAAGGTC
	109-124	consensus		cTCtCGGCCTAgTTGGGGCCCCAcgGACCCCCGGCGTAGGTCGCGtAATtTGGGTAAgGTC
	SEO ID NO	: ISOLATE		
	119	S9	267	ATCCATACCCTCACATCCCCCTTL
	117	IND3	30/. 367	ATCGATACCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCC
	118	IND8	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
		INDO	36/.	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC

111	D1	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
		307	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
112	US6	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
113	P10	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
		3.67	THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CO
114	DK1	36/	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
115	T10	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
116	SW2	267	Process Communication Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control
		36/	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
122	HK4	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
109	SA10	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
		307	ATCGATACCT CACATGCGGCT TCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
110	S45	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
123	P8	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGGCC
124	T3	367	ATECATION CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF
		36/	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCtC
120	HK3	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGLGCCC
121	HK5	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
		50,	ATCGATACCCTCACGTGCGCCTCATGGGGTACATCCCGCTCGTCGGCGCCCC
109-124	consensus		ATCGATACCCTCACaTGCGGCTTCGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCC
SEO ID NO:	<u> ISOLATE</u>		
119	S9	429	CCCTAGGGGGCGCTGCCAGGGCLCTGGCGCATGGCGTCCGGGTLCTGGAGGACGGCGTGAA
·	•	420	COLLAGO COLO COLO COLO COLO COLO COLO COLO CO
117	IND3	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCTGGAGGACGGCGTGAA
118	IND8	428	CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCTGGAGGACGGCGTGAA
111	D1	420	CCCTA CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
	_	428	CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
112	US6	428	CCCTAGGGGGCGCTGCCAGGGCCLTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
113	P10	420	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGCGTCCGGGTTCTGGAGGACGCGTGAA
114	_	420	GOTA GOOGGE TO CANGGE CLIGGEG LATGGE GT CTGGAGGACGC GTGAA
2	DK1	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
* 115	T10	428	CCCTAGGGGGCGCTGCCAGGGCtCTGGCaCATGGtGTCCGGGTTCTGGAGGACGGCGTGAA
116	SW2	420	CCCTA CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
		120	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCTGGAGGACGGCGTGAA
122	HK4	428	CCTTAGGGGGGCGtTGCCAGaGCCCTGGCaCATGGtGTCCGGGTTgTGGAGGACGGCGTGAA
. 109	SA10	428	CtTTAGGGGGCGCTGCCAGGGCCTTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
110	S45	420	CCCTACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
		428	CCCTAGGGGGCGCTGCCAGGGCCTTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
123	P8	428	CCCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTgTGGAGGACGGCGTGAA
124	Т3	428	CCLTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
		120	CCTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
120			
120	нкз	428	CCCTAGGGGGGTTGCCAGAGCCtTGGCACATGGTGTCCGGGTTCTGGAGGACGGCGTGAA
120 121	HK3 HK5	428	CCCTAGGGGGCGTTGCCAGAGCCtTGGCACATGGTGTCCGGGTTCTGGAGGACGGCGTGAA
	_	428	CCCTAGGGGGCGTTGCCAGAGCCETGGCACATGGTGTCCGGGTTCTGGAGGACGGCGTGAA CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA
121	HK5	428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA
121	_	428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA
121	HK5	428	CCCTAGGGGGCGTTGCCAGAGCCETGGCACATGGTGTCCGGGTTCTGGAGGACGGCGTGAA CCCTAGGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA CccTAGGGGGGCGTGCCAGGGCCCTGGCGCAEGGCGTCCGGGTtcTGGAGGACGGCGTGAA
121	HK5	428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA
121	HK5 consensus	428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA
121 109-124 <u>SEQ ID NO:</u>	HK5 Consensus  ISOLATE	428 428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA CccTAGGGGGGCGTGCCAGGGCcCTGGCgCAtGGcGTCCGGGTtcTGGAGGACGGCGTGAA
121	HK5 consensus	428 428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA CccTAGGGGGGCGTGCCAGGGCcCTGGCgCAtGGcGTCCGGGTtcTGGAGGACGGCGTGAA
121 109-124 <u>SEQ ID NO:</u> 119	HK5 Consensus ISOLATE S9	428 428 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CccTAGGGGGGCGTGCCAGGGCCCTGGCGCAtGGCGTCCGGGTtcTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTTTCTT
121 109-124 SEQ ID NO: 119 117	HK5 Consensus  ISOLATE S9 IND3	428 428 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTC
121 109-124 SEQ ID NO: 119 117 118	HK5 Consensus  ISOLATE S9 IND3 IND8	428 428 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTLCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTC
121 109-124 SEQ ID NO: 119 117	HK5 Consensus  ISOLATE S9 IND3	428 428 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTLCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTC
121 109-124 SEQ ID NO: 119 117 118 111	HK5 Consensus  ISOLATE S9 IND3 IND8 D1	428 428 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCCTATCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCCTATCC  LTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTTTTCT
121 109-124 SEO ID NO: 119 117 118 111 112	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6	428 428 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTGCTATCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCCTATCCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTTCTCTATCTTCCTTTTGGCTTTTGCTATCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTTCTCTTTTCCTTTTGCTTTTCCTCTTTCCTTTTCTTTTCTTTTTCTTTTTT
121 109-124 SEQ ID NO: 119 117 118 111 112 113	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10	428 428 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTGCTATCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTGCTATCC  tTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTTTTCCTCTTTTGCTTTTCCTCTTTTCCTCTTTTCCTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6	428 428 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTGCTATCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTGCTATCC  tTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTTTTCCTCTTTTGCTTTTCCTCTTTTCCTCTTTTCCTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1	428 428 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTGCTATCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTGCTATCC  tTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTACGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTTTTCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10	428 428 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTGCTATCC CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTGCTATCC CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTACGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTCTCTCTC
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1	428 428 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10	428 428 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4	428 428 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTGCTTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10	428 428 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4	428 428 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCACAGGGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45	428 428 489 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGGGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8	428 428 489 489 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTTGCTATCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTTGCTATCC  ETATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTTCTTATCTTCTCTTTTGGCTCTTTTCCTCTTTTCCTCTTTTCTTTTCTTTTTCTTTTT
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3	428 428 489 489 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTAGCTTTTGCTATCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTTGCTATCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTTCTTATCTTCCTCTTTGGCTTTTCTTTC
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8	428 428 489 489 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTAGCTTTTGCTATCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTTGCTATCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTTCTTATCTTCCTCTTTGGCTTTTCTTTC
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3	428 428 489 489 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTC
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3	428 428 489 489 489 489 489 489 489 489 489	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTAGCTTTTGCTATCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGGCTTTTGCTATCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC  CTATGCAACAGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC  CTATGCAACAGGAATTTGCCCGGTTGCTCTTTTCTTATCTTCCTCTTTGGCTTTTCTTTC
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTC
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121	HK5 CONSENSUS  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTGCTTTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121 109-124	HK5 CONSENSUS  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5 CONSENSUS	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACAGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGCTGTCC  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTC
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121 109-124 SEO ID NO: 119	HK5 CONSENSUS  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5 CONSENSUS	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGGGCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGCTGTCC  CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTC
121 109-124  SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121 109-124  SEO ID NO: 119 117	HK5 CONSENSUS  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5 CONSENSUS	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACAGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTAGCTTTGCTATCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGCC CTATGCAACAGGGAATTTGCCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTTCCCTGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAATTACCCGGTTGCCCTTTCTCTTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAATTTACCCGGTTGCCCTTTCTCTTTCTCTTTTTTCTTTTTTTT
121 109-124 SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121 109-124 SEO ID NO: 119	HK5 CONSENSUS  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5 CONSENSUS	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACAGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGGCGTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGGAGGACGGCGTGAA  CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTAGCTTTGCTATCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGCC CTATGCAACAGGGAATTTGCCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTTCCCTGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTACCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAATTACCCGGTTGCCCTTTCTCTTATCTTCCTCTTTGGCTTTTGCTGTCC  CTATGCAACAGGGAATTTACCCGGTTGCCCTTTCTCTTTCTCTTTTTTCTTTTTTTT
121 109-124  SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121 109-124  SEQ ID NO: 119 117 118	HK5 CONSENSUS  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5 CONSENSUS  ISOLATE S9 IND3 IND8	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGGGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGCTGTCC CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCCTATCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTCC CTATGCAACAGGGAATTTGCCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTGCTCC CTATGCAACAGGGAATTTGCCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCCCTTTCCTCTATCTTCCTCTTTTGCTTTTCCTTTTTTTT
121  109-124  SEO ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121 109-124  SEO ID NO: 119 117 118 111	HK5 Consensus  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5 Consensus  ISOLATE S9 IND3 IND8 D1	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGCTGTCC CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTTTT
121 109-124  SEQ ID NO: 119 117 118 111 112 113 114 115 116 122 109 110 123 124 120 121 109-124  SEQ ID NO: 119 117 118	HK5 CONSENSUS  ISOLATE S9 IND3 IND8 D1 US6 P10 DK1 T10 SW2 HK4 SA10 S45 P8 T3 HK3 HK5 CONSENSUS  ISOLATE S9 IND3 IND8	428 428 489 489 489 489 489 489 489 489 489 48	CCCTAGGGGGCGTTGCCAGGGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGGCGTGAA  CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCALGGCGTCCGGGTTCTGCTGTCC CTATGCAACAGGGAACCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCCTATCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTTGCTTTTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTCC CTATGCAACAGGGAATTTGCCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTGCTCC CTATGCAACAGGGAATTTGCCCGGTTGCCCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTGCTGTCC CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTTGGCTTTTGCTGTCC CTATGCAACAGGGAATTTACCCGGTTGCCCTTTCCTCTATCTTCCTCTTTTGCTTTTCCTTTTTTTT

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113	P10	550	TGccTGACCATCCCAGCgTCCGCT
114	DK1	550	TGTTTGACCATCCCAGCTTCCGCc
115	T10	550	TGTCTGACCATCCCAGCTTCCGCT
116	SW2	550	TGTCTGACCATCCCAGCTTCCGCT
122	HK4	550	TGTTTGACCATCCCAGCTTCCGCT
109	SA10	550	TGTTTaACCATCCCAGCTTCCGCT
110	S45	550	TGCTTGACCATCCCAGCTTCCGCT
123	. P8	550	TGtcTGACCATCCCAGCTTCCGCT
124	<b>T</b> 3	550	TGCTTGACCATCCCAGCTTCCGCT
120	нкз	550	TGCTTGACCACCCCAGCTTCCGCT
121	HK5	550	TGtcTGACCACCCCAGtTTCCGCT
109-124	consensus		TGttTgACCatcCCAGctTCCGCt

SEO ID NO	: ISOLATE	
119	S9	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
117	IND3	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
118	INDS	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCACAGG
111	D1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCCACAGG
112	US6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
113	P10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
114	DK1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
115	T10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
116	SW2	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCACAGG
122	HK4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAGACGTAACACCAACCGCCGCCCACAGG
109	SA10	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
110	S45	1 ATGAGCACGAATCCTAAACCTCAAAGACAAACCAAACGTAACACCAACCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGACAAACCAAACGTAACACCAACCGCCCCCCACAGG
123	P8	1 ATGAGCACGACTCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCCACAGG 1 ATGAGCACGACTCCTAAACCTCAAAGAAAAAACCAAACGTAACACCAACCGCCCCACAGG
124	T3	1 ATGAGCACGACTCCTAAACCTCAAAGAAAAACCAAACGTAACACCAGCCGCCGCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCCCCACAGG
120	HK3	1 ATGAGCACGAATCCTAAACCTCAAAGGAAAAACCAAACGTAACACCAACCGCCCCACAGG 1 ATGAGCACGAATCCTAAACCTCAAAGGAAAAACCAAACGTAACACCAACCGCCCCCCCC
121	HK5	
108	DR4	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCACAGG
104	US11	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
105	S14	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
106		1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
105	SW1	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
107	S18	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
į 103	DK7	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGG
103-124		<b>300.000 3.000</b>
103-124	consensus	ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGCCGCCCACAGG
- - -		
CEO ED MO		
SEO ID NO:		
119	S9	62 ACGTLAAGTTCCCGGGCGGTGGLCAGATCGTCGGTGGAGTTTACCTGTTGCCGCGCAGGGG
117	IND3	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
118	IND8	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
111	D1	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
112	US6	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
113	P10	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGGTTTACCTGTTGCCGCAGCGG
114	DK1	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
115	T10	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
116	SW2	62 ACGTCAAGTTCCCGGGCGGTGGCCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCACGCG
122	HK4	62 ACGTLAAGTTCCCGGGCGGTGGCCAGATCGTcGGTGGAGTTTACCTGTTGCCGCCACCCC
109	SA10	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTCTALCTGTTGCCGCGCAGGGG
110	S45	62 ACGTCAAGTTCCCGGGtGGcGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGG
123	P8	62 ACGTTAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
124	<b>T3</b>	62 ACGTTAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
120	HK3	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
121	HK5	62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACCTGTTGCCGCGCAGGGG
108	DR4	62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
104	US11	62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
105	S14	62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
106	SW1	62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
107	S18	62 ACGTEAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
103	DK7	62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
103-124	consensus	ACGTCAAGTTCCCGGGCGGtGGtCAGATCGTtGGTGGAGTtTAccTGTTGCCGCGCAGGGG
		The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
SEO ID NO:	<b>ISOLATE</b>	
119	S9	123 CCCCAGGTTGGGTGTGCGCGC&ACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
117	IND3	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
118	IND8	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
111	D1	123 CCC AGGTTGGTGTGGGGGGGGGTGGAAGGCTTCGGAGGGGGGGG
112	US6	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
113	P10	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
114	DK1	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
115		123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
116	T10	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
122	SW2	123 CCCCeGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
144	HK4	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG

			radora oc
109 .	SA10	122	CCCCA CCTTCCCCTCTCCCCCCA C-2 CCA 2 CTTCCCCA CCCCTCCA C-2 CCA 2 CTTCCCCA CCCCTCCA CCA 2 CTTCCCCA CCA 2 CTTCCCCA CCA 2 CTTCCCCA CCA 2 CTTCCCCA CCA 2 CTTCCCA CCA 2 CTTCCCA CCA 2 CTTCCCA 2 CTTCCA 2 CTTCCCA 2 CTTCCA 2 CTTCA 2 CTTCCA
110	S45	123	CCCCAGGTTGGGTGTGCGCGCGACGAGGAGGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
123	P8	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCaCAACCTCGTGGACGG
124	T3	123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGATCGCAACCTCGTGGCAGG
120		123	CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
121	нкз	123	CCCCAGGTTGGGTGTGCGCGCGACCAGGAAGACTTCaGAGCGGTCGCAACCTCGTGGAAGG
108	HK5 DR4	123	CCCCAGGTTGGGTGTGCGCGCGACCAGGAAGACTTCCGAGCGGTCGCAACCTCGTGGAAGG
108		123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGA
	US11	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGA
105	S14	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGA
106	SW1	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGA
107	S18	123	CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTCGCAACCTCGCGGTAGA
103	DK7	123	CCCTAGATTGGGTGTGCGCGCGGGGGGAGGAGACTTCCGAGCGTCGCAACCTCGAGGTAGA
103-124	consensus		CCCeaGgTTGGGTGTGCGCGCgaCtAGGAAGACTTCeGAGCGgTCgCAACCTCGtGGaaGg
			<b>3</b> • <b>3</b> • • • • • • • • • • • • • • • • • • •
SEQ ID N	O: ISOLATE		
119	S9	184	CGACAACCTATCCCCAAGGCTCGCCatCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
117	IND3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGTACC
118	IND8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGCACC
111	D1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGTACC
112	US6	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
113	P10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
114	DK1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
115	T10	184	CGACAGCCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCCGGGTACC
116	SW2	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGGCCTGGGCTCAGCCLGGGTACC
122	HK4	184	CGACAACCTATCCCCAAGGCTCGCCAaCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
109	SA10	184	CGACAACCTATCCCCAAGGCTCGCCAGCCCGAGGGCAGGACCTGGGCCCAGCCCGGGTACC
110	S45	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGCAGGCCTGGGCCCAGCCCGGGCAtC
123	P8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCCGAGGGTAGGGCCTGGGCTCAGCCCGGGCACC
124	Т3	184	CGACA ACCTATECTA A SCOTTOGGGCCCGGGCACGGTAGGCCTGGGCCCGGGCACC
120	нкз	194	TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE
121	HK5	104	CGACAACCTATCCCCAAGGCTCGCCaACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
108	DR4	104	CGACAACCTATCCCCAAGGCTCGCCGACCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
104	US11	104	CGTCAGCCTATCCCCAAGGCGCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
105	S14	104	CGTCAGCCTATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
106	SW1	104	CGTCAGCCTATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
107		184	CGTCAGCCTATCCCCAAGGCGCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTATC
103	S18	184	CGTCAGCCTATCCCCAAGGCGCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103	DK7	184	CGTCAGCCTATCCCCAAGGCaCGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGGTACC
103-124	consensus		CGaCAaCCTATCCCCAAGGCtCGcCggCCCGAGGGcAGGgCCTGGGCtCAGCCcGGGtAcC
SEQ ID NO	D: ISOLATE		
119	S9	245	CTTGGCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGLGG
117	IND3	245	CTTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCGEGG

SEO ID NO:	ISOLATE		
119	S9	245	CTTGGCCCCTCTAcGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGLGG
117	IND3	245	CTTGGCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
118	IND8	245	CTTGGCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
111	D1	245	CTTGGCCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
112	US6	245	CTTGGCCCCTCTATGGCAACGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
113	P10	245	CTTGGCCCCTCTATGGCAATGAGGGCLTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
114	DK1	245	CTTGGCCCCTCTATGGCAATGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGGG
115	T10	245	CTTGGCCCCTCTATGGCAATGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGtGG
116	SW2	245	CCTGGCCCCTCTATGGCAATGAGGGCATGGGATGGCTCCTGTCCCCCCGCGG
122	HK4	245	CTTGGCCCCTCTATGGCAATGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
109	SA10	245	CTTGGCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
110	S45	245	CTTGGCCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCCTGTCACCCCGTGG
123	P8	245	CTTGGCCCCTCTATGcCAATGAGGGCTTGGGGTGGGCGGGGATGGCTCCTGTCACCCCGCGG
124	<b>T</b> 3	245	CTTGGCCCCTCTATGGCGACGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
120	HK3	245	CTTGGCCCCTCTATGGCAACGAGGGCATGGGGTGGGCAGGATGGCTCCTGTCACCCCGCGG
121	HK5	245	CTTGGCCCCTCTATGGCAATGAGGGCATGGGTGGGCAGGATGGCTCCTGTCACCCCATGG
108	DR4	245	CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCcCCCCGTGG
104	US11	245	CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG
105	S14	245	CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG
106	SW1	245	CTTGGCCCCTCTATGGCAATGAGGGCTGCGGATGGCCGGGATGGCTCCTGTCCCCCCGTGG
107	S18	245	CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGGGGGGGG

103	DK7	245	CTTGGCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCLCCCCGTGG
		213	
103-124	consensus		CtTGGCCCCTCTAtGgCaAtGAGGGCttgGGgTGGGCaGGATGGCTCCTGTCaCCCCgtGG
SEO ID NO	D: ISOLATE		
119	S9	306	CTCTCGGCCTAGTTGGGGCCCCAatGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
117	IND3	306	tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGTC
118	· IND8	306	CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAACGTC
111	D1	306	CTCCCGGCCTAGTTGGGGCCCCACcGACCCCCGGCGTAGGTCGCGTAATTTGCGTAACGTC
112	US6	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGCGTAACCTC
113	P10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAACGTC
114	DK1	306	CTCTCGGCCTAGTTGGGGCCCCAacGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
115	T10	306	CTCcCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
116	SW2	306	CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCGGCGTAGGTCGCGTAATTTGCGTAACGTC
122	HK4	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAACGTC
109	SA10	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCG+AATTTGGGTAAGGTC
110	S45	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAACGTC
123	P8	306	CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
124	Т3	306	CTCCCGGCCTAATTGGGGCCCCACAGACCCCCGGCGTAGGTCGCG+AATcTGCGTAACCTC
120	HK3	306	CTCTCGGCCTAATTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGCGTAACCTC
121	HK5	306	CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCG+ A ATTTGCGTA AGGTC
108	DR4	306	CTCTCGGCCTAGCTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
104	US11	306	CTCTCGGCCTAGCTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
105	S14	306	CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTCCCGTAACGTC
106	SW1	306	CTCTCGGCCTAGCTGGGGCCCTACAGACCCCCGGCGTAGGTCGCGCAATTTCCGTAACGTC
107 103	S18	306	CTCcCGGCCTAGCTGGGGCCCTACAGACCCCCGGCGTAGGTCGCGCAATTTGGGCAAAGTC
103	DK7	306	CTCLCGGCCTAGCTGGGGCCCACAGACCCCCGGCGCAGGTCGCGCAATTTGGGLAAAGTC
103-124	consensus		cTCtCGGCCTAgtTGGGGCCCcAc-GACCCCCGGCGtAGGTCGCGtAATtTGGGtAAgGTC
000 TD 110			
SEO ID NO			
119	S9	367	ATCGATACCCTCACATGCGGCTTtGCCGACCTCATGGGGTACATtCCGCTCGTCGGCGCCC
117	IND3	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGGTACATCCCGCTCGTCGCCCCCC
118	IND8	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGCCCCCCCC
111 112	D1	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
113	US6 P10	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
114	DK1	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
115	T10	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
116	SW2	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
122	HK4	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
109	SA10	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
110	S45	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
123	P8	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
124	T3	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGGCC
120	нкз	367	ATCGATACCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCEC ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGEGCCC
121	HK5	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
108	DR4	367	ATCGACACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
104	US11	367	ATCGATACCCTLACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
105	S14	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
106	SW1	367	ATCGATACCCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
107	S18	367	ATCGATACCTCACGTGCGGCTTCGCCGACCTCATGGGGTACATTCCGCTCGTCGGCGCCC
103	DK7	367	ATCGATACCCTLACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCC
103-124	consensus		ATCGALACCCTCACaTGCGGCTTcGCCGACCTCATGGGGTACATLCCGCTCGTCGGCGCCC
SEO ID NO	TCOLEMA		
119		400	
117	S9	428	CCCTAGGGGGCGCTGCCAGGGCLCTGGCGCATGGCGTCCGGGTLCTGGAGGACGGCGTGAA
118	IND3 IND8	428	CCCTAGGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCCTGGAGGACGACGCCTCCAA
111	DI	420	CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTCCTGGAGGACGGCGTGAA
112	US6	420	CCCTAGGGGGTGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
	030	740	CCCTAGGGGGCGCTGCCAGGGCCLTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA

113	P10	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
114	DK1	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
115	T10	428	CCCTAGGGGGCGCTGCCAGGGCtCTGGCaCATGGtGTCCGGGTTCTGGAGGACGGCGTGAA
116	SW2	428	CCCTAGGGGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCTGGAGGACGGCGTGAA
122	HK4	428	CCTTAGGGGGCGTGCCAGAGCCCTGGCaCATGGLGTCCGGGTTgTGGAGGACGCGTGAA
109	SA10	428	CtTTAGGGGGCGCTGCCAGGGCCTTGGCGCATGGCGTCCGGGTTCTGGAaGACGGCGTGAA
110	S45	428	CCCTAGGGGGCGCTGCCAGAGCCTTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
123	P8	428	CCCTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTGTGGAGGACGCGTGAA
124	<b>T</b> 3	428	CCLTAGGGGGCGTTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGCGTGAA
120	HK3	428	CCCTAGGGGGCGTTGCCAGAGCCLTGGCACATGGTGTCCGGGGTTCTGGAGGACGGCGTGAA
121	HK5	428	CCCTAGGGGGCGTTGCCAGAGCCCTGGCACACGGTGTCCGGGTTCTGGAGGACGCGTGAA
108	DR4	428	CCCTEGGGGGCGCTGCCAGGGCCCTGGCGCATGCCGTCCGAGTTCTGGAAGACGCGTGAA
104	US11	428	CECTCGGaGGCGCTGCCAGGGCCCTGGCGCATGCGTCCGGGTTCTGGAAGACGCGTGAA
105	S14	428	CCTCGGGGGCGCTGCCAGGGCCCTGGCGCATGCGTCCGGGTTCTGGAAGACGCGTGAA
106	SW1	428	CTCTtGGAGGCGCTGCCAGGGCCCTGGCGCTCCGGGTTCTGGAAGACGCGTGAA
107	S18	428	CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGCGTCCGGGTTCTGGAAGACGCGTGAA
103	DK7	428	CTCTEGGAGGCGCTGCCAGGGCCCTGGCGCATGCGTCCGGGTTCTGGAAGACGCGTGAA
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
103-124	consensus		CccTaGGgGGcGcTGCCAGgGCccTGGCgCAtGGcGTCCGgGTtcTGGAgGACGGCGTGAA
SEO ID NO	)· TSOLATE		·
	J 1 1 1 1 . Δ 1 F		

- 3	113	59 489	CTATGCAACAGGGAACCTCCCGGTTGCTCTTTCTCTATCTTCCTTC
7	117	IND3 489	CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTAGCTTTGCTATCC
	118	IND8 489	CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTATCC
_	111	D1 489	tatgcaacagggaattgcccggttgctctttctctatcttcctcttggctttgctgtcc
ij	112	US6 489	CTATGCAACAGGGAACTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
	113	P10 489	CTATGCAACAGGGAATCTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
Ħ	114	DK1 489	CTACGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTCTGLTGTCC
,054 ,054	115	T10 489	CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTTTCTATCTTCCTCTTGGCTCTGCTGTCt
1	116	SW2 489	CTATGCAACAGGGAATCTGCCCGGTTGCTCCTTTTCTATCTTCCTCTTGGCTLTGCTGTCC
<del>_</del>	122	HK4 489	CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTCTGTCC
	109	SA10 489	CTATGCAACAGGGAATTTGCCCGGTTGCcCTTTCTCTATCTTCCTCTTGGCTLTGCTGTCC
===	110	S45 489	CTATGCAACAGGGAATCTGCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTCTCTCT
=== ===	123	P8 489	CTATGCAACAGGGAATCTGCCTGGTTGCTCTTTCTCTATCTTCCTLTTGGCTTTGCTGTCL
<b>#</b> [	124	, T3 489	tTACGCAACAGGGAATTTGCCTGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
U	120	HK3 489	CTALGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCTTTGCTGTCC
Ħ	121	HK5 489	CTACGCAACAGGGAATATACCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTGTCC
 Fa	108	DR4 489	CTATGCAACAGGGAATCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGGCTTTGCTCTCT
	104	US11 489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTC
Ų	105	S14 489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTCCTaGCCCTGCTTTCT
	106	SW1 489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTC
	107	S18 489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTC
	103	DK7 489	CTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATCTTCCTTLTGGCCCTGCTCTCT

103-124 consensus cTAtGCAACAGGGAAtcTgCCcGGTTGCtCtTcTCTCTCTCTCTTgGCttTGcTgTCc

SEO ID NO:	<u>ISOLATE</u>	
119	S9	550 TGTTTGACCATCCCAGCTTCCGCT
117	IND3	550 TGTTTGACCATCCCAGCTTCCGCT
118	IND8	550 TGTTTGACCGTCCCAGCTTCCGCT
111	D1	550 TGTTTGACCATCCCAGCTTCCGCT
112	US6	550 TGTTTGACCATtCCAGCTTCCGCT
113	P10	550 TGCCTGACCATCCCAGCGTCCGCT
114	DK1	550 TGTLTGACCATCCCAGCTTCCGCC
115	T10	550 TGTCTGACCATCCCAGCTTCCGCT
116	SW2	550 TGTCTGACCATCCCAGCTTCCGCT
122	HK4	550 TGTTTGACCATCCCAGCTTCCGCT
109	SA10	550 TGTTTAACCATCCCAGCTTCCGCT
110	S45	550 TGCTTGACCATCCCAGCTTCCGCT
123	P8	550 TGtcTGACCATCCCAGCTTCCGCT
124	Т3	550 TGCTTGACCATCCCAGCTTCCGCT
120	HK3	550 TGCTTGACCACCCCAGCTTCCGCT
121	HK5	550 TGtcTGACCACCCCAGtTTCCGCT

108	DR4	550	TGCtTGACCGTGCCCGCaTCgGCC
104	US11	550	TGCCTGACTGTGCCCGCTTCAGCC
105	S14	550	TGCCTGACTGTGCCCGCTTCAGCC
106	SW1	550	TGCCTGACaGTGCCCGCGTCAGCC
107	S18	550	TGLCTGACLGTGCCCGCGTCAGCL
103	DK7	550	TGcCTGACcGTGCCCGCtTCgGCc
103-124	consensus		TGttTqACcatcCCaGctTCcGCt

# FIGURE 6D

SEO ID NO:         ISOLATE           128         T2           125         T4           126         US10           127         T9           125-128         consensus           SEO ID NO:         ISOLATE           128         T2           125         T4	1 ATGAGCACAALTCCTAAACCTCAAAGAAAAACCAAAAGAAACACLAACCGTCGCCCACAAG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGTCGCCCACAAG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACCACAACCGTCGCCCACAAG 1 ATGAGCACAAATCCAAAACCCCAAAGAAAAACCALAAGAAACACCAACCGTCGCCCACAAG  ATGAGCACAAATCCLAAACCCCAAAGAAAAACCAAAAGAAACAC-AACCGTCGCCCACA-G  ATGAGCACAAATCCLAAACCCCAAAGAAAAACCAAAAGAAACAC-AACCGTCGCCCACA-G  62 ACGTTAAGTTLCCGGGCGGCGGCCAGATCGTTGGCGGGAGTATACTTGCTGCCGCGCACGGG
126 US10 127 T9	62 ACGTTAAGTTECCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG 62 ACGTTAAGTTECCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG 62 ACGTTAAGTTECCGGGCGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
125-128 consensus	ACGTTAAGTT-CCGGGCGGCCAGATCGTTGGCGGAGTATACTTGLTGCCGCGCAGGGG
SEO ID NO: ISOLATE	
128 T2	123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCLCGTGGAAGG
125 T4	123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGATCCCAGCCACGTGGGAGG
126 US10	123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCACGTGGGAGG
127 T9	123 CCCLAGGTTGGGTGTGCGCACGACAAGGAAGACTTCGGAGCGGTCCCAGCCACGTGGGAGG
125-128 consensus	CCCcAGGTTGGGTGCGCgCGACAAGGAAGACTTCGGAGCGgTCCCAGCCaCGTGGGAGG
SEO ID NO: ISOLATE	
128 T2	184 CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
125 T4	184 CGCCAGCCCATCCCLAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
126 US10	184 CGCCAGCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATALC
	184 CGCCAGCCCATCCCCAAAGATCGGCGCCCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
127 T9	184 CGCCAGCCCATCCCCAAAGATCGGCGCtCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
125-128 consensus	CGCCAGCCCATCCCCAAAGATCGGCGCtCCACTGGCAAGTCCTGGGGAAAACCAGGATAcC
SEC ID NO. ICOLAND	
SEO ID NO: ISOLATE	•
128 T2	245 CCTGGCCCCTGTATGGGAATGAGGGGCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
125 T4	245 CCTGGCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
126 US10	245 CtTGGCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCCGAGG
127 T9	245 CCTGGCCtCTATATGGGAATGAGGGACTCGGCTGGGCGGGGATGGCTCCTGTCCCCCGAGG
125-128 consensus	CcTGGCCcCT-TATGGGAATGAGGGaCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
SEO ID NO: ISOLATE	
128 T2	306 TTCtCGTCCTCtTGGGGCCCCAATGACCCCCGGCATAGGTCGCGCAAtGTGGGTAAAGTC
125 T4	306 TTCCCGTCCTCcTGGGGCCCCAATGACCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC
126 US10	306 TTCCCGTCCTCTTGGGGCCCCAcTGALCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC
127 T9	306 TTCCCGTCCTCTTGGGGCCCCAgTGACCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC
125-128 consensus	TTCcCGTCCCTCtTGGGGCCCCAaTGAcCCCCGGCATAGGTCGCGCAAcGTGGGTAAgGTC
SEC ID NO. TOOLS	
SEO ID NO: ISOLATE	367 18601816688116881
128 T2	367 ATCGATACCCTAACGTGCGGCCTTGCCGACCTCATGGGGTACaTCCCCGTCGTAGGCGCCC
125 T4	36 / ATCGATACCCTAACGTGCaGCcTTGCCGACCTCATGGGGTACaTCCCCGTCGTAGGCGaCC
126 US10	36 / ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGaTACATCCCCGTCGTGCGCCCCC
127 T9	367 ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC
125-128 consensus	ATCGATACCCTAACGTGCgGCtTTGCCGACCTCATGGGGTACaTCCCCGTCGTaGGCGccC
SEO ID NO: ISOLATE	
128 T2	428 CGcTtGGTGGtGTCGCCAGAGCTCTtGCGCATGGCGTGAGAGTCCTGGAGGACGGAGTTAA
84908 4	$\cdot$

## FIGURE 6D

125	T4	428	CGtTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA
126	US10	428	CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA
127	Т9	428	CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTGGAGGACGGGGTTAA
125-128	consensus		$\tt CGcTtGGTGGcGTcGCCAGAGCTCTcGCGCAtGGCGTGAGAGTCCTGGAGGACGGGGTTAA$
SEO ID NO	: ISOLATE		
128	T2	489	TTATGCAACAGGLAACTTACCCGGTTGCTCCTTTTCTATCTTCTTGCTaGCCCTgCTGTCC
125	<b>T4</b>	489	TTATGCAACAGGGAACTTACCEGGTTGCTCCTTTTCTATETTCTTGCTGGCCCTACTGTCC
126	US10	489	TTATGCAACAGGGAACTTACCCGGTTGCTCCTTTTCTATCTTCTTGCTGGCCLTACTGTCC
127	Т9	489	TTATGCAACAGGGAACCTACCEGGTTGCTCETTTTCTATCTTCTTGCTGGCCCTACTGTCC
125-128	consensus		TTATGCAACAGGGAACtTACC-GGTTGCTCcTTTTCTATcTTCTTGCTGGCCcTaCTGTCC
SEQ ID NO	: ISOLATE		
128	T2	550	TGCATCACtATTCCgGTtTCaGCT
125	T4	550	TGCATCACCATTCCAGTCTCGGCT
126	US10	550	TGCATCACCATTCCAGTCTCTGCT
127	Т9	550	TGCATCACCACTCCgGcCTCTGCT
125-128	consensus		TGCATCACCALTCC-GLCTCLGCT

## FIGURE 6E

SEO ID NO:         ISOLATION           131         DK1           132         SV           133         DF           129         T           130         US           129-133         consensu	1 ATGAGCACAATCCTAAACCTCAAAGAAAACCAAAAGAAATACAAACCGCCGCCCACAGG 1 ATGAGCACAATCCTAAACCTCAAAGAAAACCAAAAGAAATACAAACCGCCGCCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACAAACCGCCGCCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACAAACCGCCGCCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACAAACCGCCGCCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACCGCCGCCCACAGG
SEO ID NO: ISOLAT 131 DK1 132 SW	.1 62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGGTTTACTTGCTGCCGCGCAGGGG
133 DK	<ul> <li>62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGGTTTACTTGCTGCCGCGCAGGGG</li> <li>62 ACGTCAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGGTTTACTTGCTGCCGCGCAGGGG</li> </ul>
129-133 consensu	ACGTLAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
SEQ ID NO:         ISOLAT           131         DK1           132         SW           133         DK           129         T           130         US	123 CCCCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA 123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA 123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGLCTTCCGAGCGATCCCAGCCGCGTGGGAGG 123 CCCLAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA 123 CCCLAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
129-133 consensu	B CCCcAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
SEQ ID NO:         ISOLAT           131         DK1           132         SW           133         DK           129         T           130         US	1 184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGCCCTGGGGAAAGCCAGGATATC 3 184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAGCCAGGATATC 8 184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAACCGGGATATC 8 184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAACCAGGATATC
129-133 consensu	-
SEO ID NO:         ISOLAT           131         DK1           132         SW           133         DK           129         T           130         US	245 CTTGGCCCCTGTATGGAAACGAGGGCTGCGGCAGGTTGGCTCCTGTCCCCCGCGG 3 245 CTTGGCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG 8 245 CTTGGCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG 8 245 CTTGGCCTCTLTACGGAAACGAGGGCTGCGGLTGGGCAGGTTGGCTCCTGTCCCCCGCGG
129-133 consensu	
SEO ID NO;         ISOLAT;           131         DK1           132         SW           133         DK           129         T           130         US	306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAAATCACGCAATTTGGGTAAAGTC 306 GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAAGTC 306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAAGTC 306 GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGTAATTTGGGCAGAGTC
129-133 consensu	GTCTCgTCCTAcTTGGGGCCCCACTGACCCCCGGCALAGATCACGcAALTTGGGcAaaGTC
SEO ID NO:         ISOLATI           131         DK1:           132         SW:           133         DK6           129         T8	367 ATCGACACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTCGGCGCCC 367 ATCGACACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC 367 ATCGACACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC
84892 1	

# FIGURE 6E

130	US1	367	ATCGATACCATTACgTGTGGTTTTGCCGACCTCATGGGGGTACATCCCTGTCGTTGGCGCCC
129-133	consensus		ATCGACACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTtGGCGCCC
	_		
SEO ID N			
131	DK11	428	AVEN TO THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PR
132	SW3	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGCGATAAA
133	· DK8	428	
129	T8	428	CGGTCGGAGGCGTCGCCAGAGCTCTGGCACAtGGTGTTAGGGTCCTGGAAGACGCGATAAA
130	US1	428	CGGTCGGAGGCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
129-133	consensus		CGGTCGGAGGCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
SEO ID N	O: ISOLATE		
131	DK11	489	TTACCOA A CACCOA ATCTTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTC
132	SW3	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTTATCTTACTTGCTCTTCTGTCa
133	DK8	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTGCTCTTCTGTCG
129	T8	489	TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTTCTATCTTCTTGCTTG
130	USI	489	cTAtGCAACAGGGAATTTGCCTGGTTGCTCTTTTTTCTATCTTCTTGCTTG
-50	001	407	tTACGCAACAGGGAATCTGCCTGGTTGCTCCTTTTCTTATCTTCTTACTTGCTCTTCTGTCg
129-133	consensus		tTAcGCAACAGGGAATcTGCCTGGTTGCTCtTTTTCTTATCTTCTTACTTGCTCTTCTGTCg
SEO ID N			
131	DK11	550	TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550	TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550	TGCTgCACAGTGCCAGTGTCTGCG
129	<b>T8</b>	550	TGCTECACAGTGCCAGTGTCTGCA
130	US1	550	TGCgcCACgGTGTCTGCA
129-133	consensus		TGCt - CACaGTGCCaGTGTCTGCg

#### FIGURE 6F

SEO ID NO:	<u> ISOLATE</u>	
131	DK11	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCCGCCCACAGG
132	SW3	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAATACAAACCGCCGCCCACAGG
133	DK8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACCACAAACCGCCGCCCACAGG
129	TSC	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACCACAAACCGCCGCCCACAGG
130 125	US1 T4	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACAAACCGCCGCCCACAGG 1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACCAACCGTCGCCCACAGG
126	US10	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCGACCG
127	T9	1 ATGAGCACAAATCCAAAACCCCAAAGAAAAACCALAAGAAACACCAACCGTCGCCCACAGG
128	T2	1 ATGAGCACAALTCCTAAACCTCAAAGAAAAACCAAAAGAAACACTAACCGTCGCCCACAAG
134	S83	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACTAACCGcCGCCCACAGG
125-134	consensus	ATGAGCACAAATCCLAAACCLCAAAGAAAAACCAAAAGAAACACAAACCGcCGCCCACAgG
SEO ID NO:	<u> ISOLATE</u>	
131	DK11	62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
132	SW3	62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGGAGTTTACTTGCTGCCGCGCAGGGG
133 129	DK8 T8	62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGGAGTTTACTTGCTGCCGCGCAGGGG
130	USI	62 ACGTCAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGGTTTACTTGCTGCCGCGCAGGGG 62 ACGTCAAGTTCCCGGGTGGCGGLCAGATCGTTGGCGGAGGTTTACTTGCTGCCGCGCAGGGG
125	T4	62 ACGTTAAGTTCCCGGGCGGCCAGATCGTTGGCGGAGGTTTACTTGTTGCCGCGCAGGGG
126	USIO	62 ACGTTAAGTTECCGGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
 ↑ 127	Т9	62 ACGTTAAGTTcCCGGGCGGCCAGATCGTTGGCGGAGTATACTTGTTGCCGCGCAGGGG
128	T2	62 ACGTTAAGTTECCGGGCGGCCAGATCGTTGGCGGAGGTATACTTGCTGCCGCGCAGGGG
134	S83	62 ACGTCAAGTTCCCGGGCGGLGGCCAGATCGTTGGCGGAGTATACTTGCTGCCGCGCAGGGG
⊊ ⊑ 125-134	consensus	ACGTLAAGTTcCCGGG-GGcGGCCAGATCGTTGGCGGAGT-TACTTGcTGCCGCGCAGGGG
m 113 131 (	COMBCMBUB	ACOT EARST TO COOK OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF CONTROL OF
; ; Fig.		
SEO ID NO:	ISOLATE	•
= 131	DK11	123 CCCCAGGTTGGGTGTGCGCACGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
132	SW3	123 CCCCAGGTTGGGTGTGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
133	DK8	123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGtCTTCCGAGCGATCCCAGCCGCGTGGGAGG
129	T8	123 CCCLAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
130	US1	123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCGTGGGAGA
∄ 125 ≒ 126	T4	123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGATCCCAGCCACGTGGGAGG
: 126 ≒ 127	US10 T9	123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCACGTGGGAGG
· 100	T2	123 CCCLAGGTTGGGTGTGCGCACGACAAGGAAGACTTCGGAGCGGTCCCAGCCACGTGGGAGG 123 CCCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCGGAGCGGTCCCAGCCLCGTGGAAGG
134	S83	123 CCCGAGATTGGGTGTGCGCGCGACGAGGAAAACTTCGGAACGGTCCCAGCCCAGCCGGGAGGGA
125-134	consensus	CCCcAGgTTGGGTGTGCGCGCGACaAGGAAgaCTTCcGAgCGaTCCCAGCCgCGTGGgAGg
CEO TO TO	7007155	
<u>SEO ID NO:</u> 131	<u>ISOLATE</u> DK11	104 CCCCACCCCAMCCCCAAAACAMCCCCCCCCCCCCACAAAAAA
132		184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGCCCTGGGGAAAGCCAGGATATC
133	SW3 DK8	184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAGCCAGGATATC 184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAACCgGGATATC
129	T8	184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAACCGGGATATC
130	USI	184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCCTGGGGAAAGCCAGGATATC
125	T4	184 CGCCAGCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATATC
126	US10	184 CGCCAGCCCATCCCCAAAGATCGGCGCCCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
127	Т9	184 CGCCAGCCCATCCCCAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
128	T2	184 CGCCAGCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCCTGGGGAAAACCAGGATACC
134	S83	184 CGCCAGCCCATCCCTAAAGATCGGCGCACCACTGGCAAGTCCTGGGGAAGGCCAGGATACC
125-134	consensus	CGCCAGCCCATCCCgAAAGATCGGCGCtCCAC-GGCAAGtCCTGGGGAAaaCCaGGATAtC
SEO ID NO:	ISOLATE	
131	DK11	245 CTTGGCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCCGCGG
132	SW3	245 CTTGGCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCCGCGG
133	DK8	245 CTTGGCCCCTGTATGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCGCGG
129	<b>T8</b>	245 CTTGGCCTCTETACGGAAACGAGGGCTGCGGETGGGCAGGTTGGCTCCTGTCCCCCGCGG

# FIGURE 6F

US1	245	CTTGGCCTCTGTACGGAAACGAGGGCTGCGGCTGGGCAGGTTGGCTCCTGTCCCCCCGCGG
	243	CITGGCTCTGTACGGAAACGAGGGCTGGGCAGGTTGGCTCCTGTCCCCCCGCGG
<b>T4</b>	245	CCTGGCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
US10	245	CETGGCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
	245	CONCOCCE OTHER WOODS AND ADDRESS OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPER
	245	CCTGGCCLCTATATGGGAATGAGGGACTCGGCTGGGCGGGGATGGCTCCTGTCCCCCGAGG
	245	CCTGGCCCCTGTATGGGAATGAGGGGCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
583	245	CLTGGCCCCTGTATGGGAATGAGGGCCTCGGCTGGGCAGGGTGGCTCCTGTCCCCCCGCGG
505	,	cerocecororation and the control of the cerocal control of the cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cerocal cero
consensus		CtTGGCCcCTgTAtGG-AA-GAGGGcCGGcTGGGCaGGtTGGCTCCTGTCCCCCGcGG
	`	
		·
		· · · · · · · · · · · · · · · · · · ·
): ISOLATE		
DK11	306	GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATABATCACGCAATTTGGGLAAAGTC
	306	CTCTCA TCCTA ATTCCCCCCCCA CTCA CCCCCCA CTCA CACCA CTCA CCCCA CTCA CTCA CCCCA CTCA CTCA CCCCA CTCA C
	306	GTCTCATCCTAATTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAAGTC
DK8	306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGCAATTTGGGCAAAGTC
T8	306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCATAGATCACGTAATTTGGGCAGAGTC
	306	GTCTCGTCCTACTTGGGGCCCCACTGACCCCCGGCACAGATCACGTAACTTGGGCAAGGTC
	300	GTCTCGTCCTACTGGGCCCCACTGACCCCCGGCACAGATCACGTAACTTGGGCAAGGTC
T4	306	TTCCCGTCCCTCGGGGCCCCAaTGACCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC
US10	306	TTCCCGTCCCTCTTGGGGCCCCAcTGAtCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC
TO	306	TTCCCGTCCCTCTTGGGGCCCCAgTGACCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC
	300	11CCCG1CC1C1TGGGGCCCCAGTGACCCCCGGCATAGGTCGCGCAACGTGGGTAAGGTC
	306	TTCTCGTCCCTCTTGGGGCCCCAaTGACCCCCGGCATAGGTCGCGCAALGTGGGTAAAGTC
S83	306	TTCTCGcCCtTCaTGGGGCCCCAccGACCCCCGGCATAaaTCGCGCAActTGGGTAAgGTC
		MG-1-G-1-G-1
consensus		-TCtCgtCCt-ctTGGGGCCCCActGAcCCCCGGCAtAgaTC-CGcAA-tTGGGtAa-GTC
		•
. TOOTSON		
DK11	367	ATCGACACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTcGGCGCCC
SW3	367	ATCGACACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC
	367	ATCOME ACCUTACION OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF
	36/	ATCGACACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC
T8	367	ATCGATACCATTACaTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC
US1	367	ATCGATACCATTACGTGTGGTTTTGCCGACCTCATGGGGTACATCCCTGTCGTTGGCGCCC
T4	367	ATCGATACCCTAACGTGCaGCcTTGCCGACCTCATGGGGTACGTCCCCGTCGTaGGCGCCC
		AIUGATAUUTAAUGIGUGUIGUUGUUGAUUTUATUGGGTAAAAAAAAAA
	507	The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
USIO	367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTGGGCGCCCC
US10	367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTGGGCGCCCC
US10 T9	367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTGGGCGCtC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTACGCGCCC
US10 T9 T2	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCLC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC
US10 T9	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCLC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC
US10 T9 T2	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTGGGCGCtC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTACGCGCCC
US10 T9 T2 S83	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCLC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATACCCGTCGTLGGCGCCC
US10 T9 T2	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCLC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC
US10 T9 T2 S83	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCLC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATACCCGTCGTLGGCGCCC
US10 T9 T2 S83	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCLC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATACCCGTCGTLGGCGCCC
US10 T9 T2 S83 Consensus	367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCLC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATACCCGTCGTLGGCGCCC
US10 T9 T2 S83 Consensus	367 367 367 367	ATCGATACCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCEC ATCGATACCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGETTTGCCGACCTCATGGGGTACATACCCGTCGTEGGCGCCC ATCGALACC-T-ACGTG-GGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC
US10 T9 T2 S83 Consensus : ISOLATE DK11	367 367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTLGGCGCCC ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC CGGTCGGAGGCGCCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus	367 367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTLGGCGCCC ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC CGGTCGGAGGCGCCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3	367 367 367 367	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATACCCGTCGTLGGCGCCC ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8	367 367 367 367 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8	367 367 367 367 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC ATCGATACCCTAACGTG-GGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1	367 367 367 367 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC ATCGATACCCTAACGTG-GGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8	367 367 367 367 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC ATCGATACCCTAACGTG-GGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4	367 367 367 367 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  ATCGALACC-T-ACGTG-GGLETTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCCCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCCCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCCCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCCCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCCCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10	367 367 367 367 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  ATCGALACC-T-ACGTG-GGLETTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCATGGCGTTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTAGGGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTAGGGTCCTTGGAGGACGGGGTTAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9	367 367 367 367 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  ATCGALACC-T-ACGTG-GGLETTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGCTCGGAGGCGTCGCCAGAGCTCTCGCGCATGGCGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGAGTCCTGGAGGACGGGGTTAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10	367 367 367 367 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  ATCGALACC-T-ACGTG-GGLETTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGCTCGGAGGCGTCGCCAGAGCTCTCGCGCATGGCGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGAGTCCTGGAGGACGGGGTTAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9	367 367 367 367 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  ATCGALACC-T-ACGTG-GGLETTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCATGGCGTTGAGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTCGCCCAGAGCTCTCCGCGCATGGCGTTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCCACGCCGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCCGCCACGCCGTGAGAGTCCTTGGAGGACGGGGTTAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9	367 367 367 367 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  ATCGALACC-T-ACGTG-GGLETTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGCTCGGAGGCGTCGCCAGAGCTCTCGCGCATGGCGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGAGTCCTGGAGGACGGGGTTAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83	367 367 367 367 428 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCACACGGTGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCTCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTGGC
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9	367 367 367 367 428 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCACACGGTGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCTCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTGGC
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83	367 367 367 367 428 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  ATCGALACC-T-ACGTG-GGLETTGCCGACCTCATGGGGTACATCCC-GTCGTtGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCATGGCGTTGAGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCCGCGCATGGCGTTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTCGCCCAGAGCTCTCCGCGCATGGCGTTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCGCACGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCGCCACGCCGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCAGAGCTCTCCCGCCACGCCGTGAGAGTCCTTGGAGGACGGGGTTAA
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83	367 367 367 367 428 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCACACGGTGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCTCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTGGC
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus	367 367 367 367 428 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCACACGGTGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCTCTCCGCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCTCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTTGCCCAGAGCCCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTTGGTGGCGTGGC
US10 T9 T2 S83 Consensus  : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus	367 367 367 367 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGETTTGCCGACCTCATGGGGTACATCCC-GTCGTEGGCGCCC  ATCGALACC-T-ACgTG-gGELTTGCCGACCTCATGGGGTACATCCC-GTCGTEGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGGTCTTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGGCGTGAGGCTCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCAGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGGCGTGAGGCTCTGGAGGACGGAGGACGGAGTAAA CGGTTGGTGGCGTGGC
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus	367 367 367 367 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGETTTGCCGACCTCATGGGGTACATCCC-GTCGTEGGCGCCC  ATCGALACC-T-ACgTG-gGELTTGCCGACCTCATGGGGTACATCCC-GTCGTEGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCCCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGGTCTTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGGCGTGAGGCTCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCAGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGGCGTGAGGCTCTGGAGGACGGAGGACGGAGTAAA CGGTTGGTGGCGTGGC
US10 T9 T2 S83 Consensus  : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus : ISOLATE DK11	367 367 367 367 428 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATCCCGTCGTLGGCGCCC  ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTLGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTTGGAGGCGTCGCCAGAGCTCTCGCCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGGGTCCTGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTTAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
US10 T9 T2 S83 Consensus  : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3	367 367 367 367 428 428 428 428 428 428 428 428 428 428	ATCGATACCTAACGTGCGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTTGGCGCCC ATCGATACCCTAACGTGCGGLTTTGCCGACCTCATGGGGTACATCCCGTCGTLGGCGCCC  ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTLGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTLGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTLGCCAGAGCTCTCGCGCACGGCGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTLGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTLGCCAGAGCTCTCGCCCATGGCGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTLGCCAGAGCTCTTCGCCCATGGGTGAGAGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTLGCCAGAGCTCTTCGCCCATGGGTTAGAGGTCCTTGGAGGACGGGGTTAA CGCTTGGTGGCGTLGCCAGAGCTCTTCGCCCATGGGTTAGAGGTCCTTGGAGGACGGGGTTAA CGGTTGGTGGCGCCAGAGCCCTTGCCCATGGGTTAGGGTTCTTGGAGGACGGGGTTAA CTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTACTTCTTCTTCTTCTTCTTCTT
US10 T9 T2 S83 Consensus  : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8	367 367 367 367 428 428 428 428 428 428 428 428 428 428	ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGGCGCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATACCCGTCGTLGGCGCCC ATCGATACCCTAACGTGCGGLTTGCCGACCTCATGGGGTACATACCCGTCGTLGGCGCCC  ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAAGATCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAAGATCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAAGATCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTTGCGCATGGCGTGAAGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCTCTTGCGCATGGCGTGAAGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCTCTTGCCGCATGGGGTGAAGGTCCTGGAGGACGGGGTTAA CGGTTGGTGGCGTCGCCAGAGCTCTTGCCCATGGGGTGAAGGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTTGCCCATGGGGTGAAGGTCCTTGAAGACGGGATTAA CTTTCGCCAACAGGAATCTGCCTGGTTGCTCTTTTTCTACTTCTTTCT
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US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4	367 367 367 428 428 428 428 428 428 428 428 428 428	ATCGATACCTAACGTGCGCTTTGCCGACCTCATGGGATACATCCCCGTCGTGGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCGTCGTCGTCGCGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCC-GTCGTCGCGCCC  ATCGALACC-T-ACGTG-GGLLTTGCCGACCTCATGGGGTACATCCC-GTCGTLGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAGACCGGGATAAA CGGTTGGTGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAGACCGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCTCTGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTTGCCCATGGGGTGAGAGTCCTGGAGACAGGGATAAA CCGTTGGTGGCGCAGAGCCCTGGCCCATGGGGTGAAGGTCCTGGAGAGCCGGGGTTAA CCGTTGGTGGCGCAGAGCCCTGGCCCATGGGGTGAGAGTCCTTGGAGACAGGGAATAA  CTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTATCTTCTTTCT
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US10 T9 T2 S83 Consensus  : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus	367 367 367 428 428 428 428 428 428 428 428 428 428	ATCGATACCTAACGTGCGCTTTGCCGACCTCATGGGATACATCCCGTCGTAGGGCGCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGGGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGGGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATACCCGTCGTTGGCGCCC  ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATACCCGTCGTTGGCGCCC  ATCGATACCCTAACGTGCAGCTCTGCCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCACACGGTGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTTGCCCCATGGGGTGAGAGTCCTTGGAGGACGGGATAAA CTACCCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTTACTTTCTTT
US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83	367 367 367 428 428 428 428 428 428 428 428 428 428	ATCGATACCTAACGTGCGCTTTGCCGACCTCATGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGCTTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGTTTTGCCGACCTCATGGGGTACATACCCGTCGTTGGCGCCC  ATCGATACCCTAACGTGCGGTTTTGCCGACCTCATGGGGTACATACCCGTCGTTGGCGCCC  CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCTCTCGCCCATGGGGTAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGAGCCGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTTGCCCATTGCTTCTTCTTTCT
US10 T9 T2 S83 Consensus  : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus : ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 Consensus	367 367 367 428 428 428 428 428 428 428 428 428 428	ATCGATACCTAACGTGCGCTTTGCCGACCTCATGGGATACATCCCGTCGTAGGGCGCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGGGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGGGCCC ATCGATACCCTAACGTGCGGCTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATCCCCGTCGTAGGCGCCC ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATACCCGTCGTTGGCGCCC  ATCGATACCCTAACGTGCGGTTTGCCGACCTCATGGGGTACATACCCGTCGTTGGCGCCC  ATCGATACCCTAACGTGCAGCTCTGCCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA CGGTCGGAGGCGTCGCCAGAGCTCTCGCGCACACGGTGTTAGGGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTCGCCCATGGGGTGAGAGTCCTGGAGGACGGGGTTAA CCGTTGGTGGCGTCGCCAGAGCCCTTGCCCCATGGGGTGAGAGTCCTTGGAGGACGGGATAAA CTACCCAACAGGGAATCTGCCTGGTTGCTCTTTTTCTTACTTTCTTT
	US10 T9 T2 S83 CONSENSUS D: ISOLATE DK11 SW3 DK8 T8 US1 T4 US10 T9 T2 S83 CONSENSUS CONSENSUS D: ISOLATE DK11 SW3 DK8 T8 US1	US10 245 T9 245 T9 245 T2 245 S83 245  CONSENSUS  D: ISOLATE DK11 306 SW3 306 DK8 306 T8 306 US1 306 US1 306 T9 306 T9 306 T9 306 S83 306  CONSENSUS  CONSENSUS  DK11 367 SW3 367 DK8 367 DK8 367 US1 367 US1 367

## FIGURE 6F

134	S83	489	${\tt TTATGCAACgGGgAAtTTgCCCGGTTGCTCtTTcTCTATCTTtcTcttgGCCCTctTgTCt}$
125-134	consensus		tTAtGCAACaGGgAAttTgCCtGGTTGCTCtTTtTCTATcTTctTgcTtGC-cTtcTGTCc
SEO ID NO	: ISOLATE		
131	DK11	550	TGCTqCACAGTGCCAGTGTCTGCG
132	SW3	550	TGCTECACAGTGCCAGTGTCTGCG
133	DK8	550	TGCTqCACAGTGCCAGTGTCTGCG
129	<b>T8</b>	550	TGCTECACAGTGCCAGTGTCTGCA
130	US1	550	TGCgcCACgGTGCCgGTGTCTGCA
125	T4	550	TGCATCACCATTCCAGTCTCcGCT
126	US10	550	TGCATCACCATTCCAGTCTCTGCT
127	Т9	550	TGCATCACCACTCCGGCCTCTGCT
128	T2	550	TGCATCACTATTCCGGTTTCaGCT
134	S83	550	TGCATCtCTgTgCCaGTTTCcGCc
125-134	consensus		TGCatCaCagtgCCaGtgTCtGCt

## FIGURE 6G

CDO TO NO TOOTAGE	
SEO ID NO: ISOLATE	1 2000000000000000000000000000000000000
138 DK12 135 HK10	1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAAGAAACACCATCCGTCGCCCACAGG
	1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAAGAAACACCATCCGTCGCCCACAGG
136 S52 137 S2	1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAAGAAACACCATCCGTCGCCCACAGG
137 52	1 ATGAGCACACTTCCTAAACCTCAAAGAAAACCAAAAGAAACACCATCCGTCGCCCACAGG
135-138 consensus	ATGAGCACACTTCCTAAACCTCAAAGAAAACCAAAAGAAACACCATCCGTCGCCCACAGG
SEO ID NO: ISOLATE	
138 DK12	62 ACGTCAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
135 HK10	62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
136 S52	62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
137 S2	62 ACATCAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
135 130	10-20-20-20-20-20-20-20-20-20-20-20-20-20
135-138 consensus	ACgT-AAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
SEO ID NO: ISOLATE	
138 DK12	123 CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCaCAGCCTCGCGGACGG
135 HK10	123 CCCACGATTGGGTGTGCGCGCGCGTAAAACTTCTGAACGGTCGCAGCCTCGCGGACGG
136 S52	123 CCCACGATTGGGTGTGCGCGCGCGCGTAAAACTTCTGAACGGTCACAGCCTCGCGGACGA
□ 137 S2	123 CCCACGATTGGGTGTGCGCGCGCGCGTAAAACTTCTGAACGGTCACAGCCTCGCGGACGG
	The second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second secon
135-138 consensus	CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCaCAGCCTCGCGGACG-
SEO ID NO: ISOLATE	
而 138 DK12	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCCTGGGCTCAGCCLGGGTACC
132 HKIU	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCCTGGGCTCAGCCCGGTACC
,	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCCTGGGCTCAGCCCGGGTACC
<u>137</u> S2	184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGATCCTGGGCTCAGCCCGGGTACC
= 135-138 consensus	CC1C1CCCTTTTCCCCTTTCCCCTTTCCTTTCCTTTCC
	CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCCTGGGCTCAGCCcGGGTACC
	CGALAGCCTATCCCCAAGGCGCGTCGGAGCCGAAGGCCGGTCCTGGGCTCAGCCGGGTACC
	CGALAGCCTATCCCCAAGGCGCGTCGGAGGCCGGTCCTGGGCTCAGCCcGGGTACC
U U U <u>seo id no:</u> isolate	
US SEO ID NO: ISOLATE TO 138 DK12	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG
☐ SEO ID NO: ISOLATE ☐ 138 DK12 ☐ 135 HK10 ☐ 136 S52	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG
口	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCG
☐ SEO ID NO: ISOLATE ☐ 138 DK12 ☐ 135 HK10 ☐ 136 S52 ☐ 137 S2	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG
□	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG
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SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2 135-138 Consensus	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG
SEO ID NO: ISOLATE   138	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG
SEO ID NO: ISOLATE   138	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCGCCCCTCTATGGTAACGAGGCTGCGGGTGGGCAGGTTGCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGGTCCCGCAATTTGGGTAAGGTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAACGAGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAGGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGGTCCCGCAATTTGGGTAAGGTC
SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2 135-138 CONSENSUS  SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2	CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGACGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAACGAGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAGGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC
SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2 135-138 CONSENSUS  SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2	CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGACGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC
SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2 135-138 CONSENSUS  SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2	CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCCCTCTATGGTAACGAGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGACGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC
SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2 135-138 CONSENSUS  SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2 135-138 CONSENSUS  SEO ID NO: ISOLATE 138 DK12 135 HK10 136 S52 137 S2 135-138 CONSENSUS	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 246 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGAGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGAGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGAGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGAGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGAGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGAGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGGGGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGGGGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGGGGGTCCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGGGGGGTCCCCGCAATTTGGGTAAAGTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGCAGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGGGGTACATCCCGCTCGTCGGCGCCTC 367 ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGTCGCGCCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAGGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGGGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAACGAGGCCCCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGGGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGGGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  367 ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAACGAGGCCCCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGGGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGGGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  367 ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  367 ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 246 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 247 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG 248 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAGGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  367 ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
SEO ID NO: ISOLATE   138	245 CTTGGCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGATGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG 245 CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  CTTGGCCCCTCTATGGTAALGAGGGCTGCGGGTGGGCAGGTGGCTCCTGTCCCCACGCGG  306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGACGTCCCGCAATTTGGGTAAAGTC 306 CTCCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  CTCCCGTCCATCTTGGGGCCCAAALGACCCCCGGCGGAGGTCCCGCAATTTGGGTAAAGTC  367 ATCGATACCCTCACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC 367 ATCGATACCCTTACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC

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#### FIGURE 6G

135	HK10 42	8 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
136	S52 42	8 CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
137	S2 42	
135-138 cor	nsensus	CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
SEO ID NO:	SOLATE	
138 .	DK12 48	
135	HK10 48	TTTCGCAACAGGGAACTTGCCCGGTTGCTCCTTTTCTATCTTCCTTC
136	S52 48	
137	- S2 48	
135-138 cor	sensus	TTT-GCAACAGGGAACTTGCCCGGTTGCTCcTTTTCTATCTTCCTTCTTGCtCTGTTCTCt
	SOLATE	
138	DK12 55	O TGCcTAATTCATCCAGCAGCTAGT
135	HK10 55	TGCTTAATTCATCCAGCAGCTAGT
136	S52 55	TGCTTAgTTCATCCtGCAGCTAGT
137	S2 55	
		2 IOCITAGII CAICCAGCAGCIAGI
135-138 con	sensus	TGCtTAaTTCATCCaGCAGCTAGT

# FIGURE 6H

SEO ID NO:	<b>ISOLATE</b>	
145	DK13	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCAATGG
143	<b>Z</b> 6	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCCATGG
144	Z7	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCCATGG
140	Z8	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCLATGG
139 142	Z4 Z5	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCCATGG
142	25 21	1 ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCCATGG
	21	1 ATGAGCACAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGECGCCCCATGG
139-145	consensus	ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGcCGCCCCATGG
SEO ID NO:	ISOLATE	
145	DK13	62 ACGTTAAGTTCCCGGGTGGCGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGG
143	26	62 ACGTTAAGTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGGTTTACTTGTTGCCGCGCAGGGG
144	27	62 ACGTTAAGTTCCCGGGCGGTGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGG
140	<b>Z8</b>	62 Atgtaaattcccaggcggcggccagatcgttggcggagtttacttgttgccgcgcaggg
139	<b>Z4</b>	62 AcGTAAAgTTCCCGGGTGGTGGCCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGG
142	<b>Z</b> 5	62 ATGTAAAATTCCCGGGTGGTGGLCAGATCGTTGGCGGAGGTTTACTTGTTGCCGCGCAGGGG
141	<b>Z1</b>	62 ATGTGAAATTCCCGGGGGGGGGCAGATCGTTGGCGGAGTTTACTTGCTGCCGCGCAGGGG
139-145	consensus	AcGT-AAgTTCCCgGGtGGtGGcCAGATCGTTGGCGGAGTTTACTTGtTGCCGCGCAGGGG
000 TD 110		
<u>SEO ID NO:</u> 145	<u>ISOLATE</u> DK13	122 CCC+2C+mmcccmcmcccaaaaaaaaaaaaaaaaaaaaaaaaaaa
143	Z6	123 CCCLAGATTGGGTGTGCGCGCGACTAGGAAGACTTCGGAGCGGTCGCAACCTCGTGGGAGG
144	26 27	123 CCCCAGGTTGGGTGTGCGCGCGACTAGGAAGACTTCGGAGCGGTCGCAACCTCGTGGGAGA
140	Z8	123 CCCCAGATTGGGTGTGCGCACACTAGGAAGACTTCGGAGCGGTCGCAACCTCGTGGGAGA
139	Z4	123 CCCCAGGTTGGGTGTGCGCGCGACTCGGAAGACTTCGGAGCGGTCGCAACCTCGTGGCAGG 123 CCCCAGGTTGGGTGTGCGCGCGACTCGAAGACTTCGGAGCGGTCGCAACCTCGTGGCAGG
142	<b>Z</b> 5	123 CCCCAGGTTGGGTGTGCGCGCGACTCGGAAGACTTCGGAGCGGTCGCAACCTCGTGGCAGG
141	Zl	123 CCCCeGGTTGGGTGTGCGCAGCTCGGAAGACTTCGGAGCGGTCaCAACCTCGEGGCAGG
139-145 c	consensus	CCCcaGgTTGGGTGTGCGCgCgaCTcGgAAGACTTCGGAGCGGTCgCAACCTCGtGGCAGg
SEO ID NO:	ISOLATE	
145	DK13	184 CGCCAGCCTATCCCCAAGGCgCGCCAACtcGAGGGtAGGTCCTGGGCTCAGCCtGGGTATC
143	<b>Z</b> 6	184 CGCCAGCCTATCCCCAAGGCACGTCGATCTGAGGGAAGGTCCTGGGCTCAGCCCGGGTATC
144	<b>Z</b> 7	184 CGTCAGCCTATCCCCAAGGCACGTCGATCTGAGGGAAGGTCCTGGGCTCAACCCGGCTACC
140	<b>Z8</b>	184 CGTCAGCCTATCCCCAAGGCACGTCGGTCcGAGGGCLAGGTCCTGGGCTCAGCCCGCTACC
139	<b>Z4</b>	184 CGTCAaCCTATCCCCAAGGCqCGcCaGcCaGAGGGCAGaTCCTGGGCgCaCAGCCCGCTACC
142	<b>Z</b> 5	184 CGTCAGCCTATCCCCCAGGCaCGtCGGTCCGAGGGCAGGTCCTGGGCTCAGCCCGGGTACC
141	<b>Z</b> 1	184 CGTCAGCCTATCCCCAAGGCGCGGCCGGTCCGAGGGCAGGTCCTGGGCTCAGCCCGGGTACC
139-145 c	onsensus	CGtCAgCCTATCCCCaAGGCaCGtCggtccGAGGGcAGgTCCTGGGCtCAgCCcGGGTAcC
		3 - 3 - 2 - 2 - 2 - 2 - 2 - 2 - 2 - 2 -
CEO TO NO	TCO1 200	
SEO ID NO:	<u>ISOLATE</u> DK13	245 CHTCCCC+CTTTT 000+1150+100
143	Z6	245 CtTGGCCcCTTTACGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCACCCCGTGG
144	20 27	245 CATGGCCTCTTTACGGTAATGAGGGTTGCGGGTGGGCGGGATGGCTCCTGTCACCCCGTGG
140	Z8	245 CATGGCCTCTTTACGGTAACGAGGGTTGCGGGTGGGCAGGATGGCTCtTGTCACCCCGTGG
139	24	245 CATGGCCTCTTTACGGTAATGAAGGCTGtGGGTGGGCAGGtTGGCTCCTGTCcCCCCGCGG
142	Z5	245 CTTGGCCcCTcTATGGCAATGAGGGCTGGGGTGGGCAGGGTGGCTCCTGTCCCCCGCGG 245 CTTGGCCCCTTTATGGCAATGAGGGCTGTGGGTGGGCAGGGTGGCTCCTGTCCCCCCGCGG
141	Z1	245 CTTGGCCCTTTACGCAATGAGGGCTGTGGGTGGGTGGGTG
		======================================
139-145 c	onsensus	CtTGGCCtCTtTAcGGcAAtGAgGGcTGcGGGTGGGCaGG-TGGCTCcTGTC-CCcCGcGG
•		
SEO ID NO:	<b>ISOLATE</b>	
145	DK13	306 CTCTCGgCCGTCTTGGGGCCCGAATGATCCCCGGCGGAGGTCCCGCAACTTGGGTAAGGTC
143	26	306 CTCTCGACCGTCTTGGGGtCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGCGTAAGGTC
144	27	306 CTCTCGACCGTCTTGGGGCCCAAATGATCCCCGGCGAAGGTCCCGCAACTTGGGTAAGGTC
140	28	306 CTCTCGACCGTCTTGGGGCCCAAATGATCCCCGGCGGAGGTCGCGCAATTTGGGTAAGGTC

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#### FIGURE 6H

139	24	306	CTCTCGGCCATCTTGGGGCCCAAATGATCCCCGGCGGAGATCGCGCAATCTGGGTAAGGTC
142	Z5	306	aTCTCGGCCATCTTGGGGCCAAATGATCCCCGGCGTAGGTCCCGCAATCTGGGTAAGGTC
141	Z1	306	tTCcaGGCCgTCTTGGGGCCccAATGATCCCCGGCGTAGGTCCCGtAATCTGGGTAAGGTC
			or a second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second seco
139-145	consensus		cTCtcGgCCgTCTTGGGGcCcaAATGATCCCCGGCGAGgTCcCGcAAttTGGGTAAgGTC
SEO ID N			
145	DK13	367	ATCGATACCCTAACTTGCGGCTTCGCCGACCTCATGGGATACATCCCGGTCGTAGGCGCCC
143	26	367	ATCGATACtCTAACTTGCGGtTTCGCCGAtCTCATGGGGTACATCCCGCTCGTAGGCGCCC
144	<b>Z</b> 7	367	ATCGATACCCTAACCTGCGGCTTtGCCGACCTCATGGGGATACATCCCGCTCGTAGGCGCCC
140	<b>Z8</b>	367	ATCGATACCCTcACGTGCGGCTTCGCCGACCTCATGGGATACATCCCGCTCGTGGGCGCCC
139	<b>Z4</b>	367	ATCGATACCCTGACGTGCGGCTTCGCCGACCTCATGGGATACATCCCGaTCGTGGGCGCCC
142	25	367	ATCGATACCCTGACGTGTGGCTTCGCCGACCTCATGGGGATACATTCCGCTCGTCGCCCCC
141	<b>Z1</b>	367	ATCGATACCCTGACGTGTGGCTTCGCCGACCTCATGGGATACATTCCGCTCGTaGGCGCCC
139-145	consensus		ATCGATACCCT-ACgTGcGGcTTcGCCGAcCTCATGGGATACATcCCGcTCGTaGGCGCCC
000 TD 17			
SEO ID NO			
145	DK13	428	CCGTGGGtGGCGTCGCCAGaGCCCTGGCGCATGGCGTCAGGCtTcTGGAGGACGGGGTCAA
143	<b>Z6</b>	428	CCGTGGGCGCGTCGCCAGGGCCCTGGCaCATGGtGTTAGGGCTGTGGAGGACGCGTCAA
144	27	428	CCGTGGGCGCCCCAGGGCCCTaGCGCATGGCGTTAGGGCTCTGGAGGACGGGATLAA
140	<b>Z</b> 8	428	Cagtaggaggcgtcgccagagccctggcgcatggcgtcagggctgtggaggacgggatcaa
139	<b>Z4</b>	428	CcGTgGGgGGCGTCGCCAGGGCtCTGGCGCATGGCGTCAGGGCTGTGGAGGACGGAT+AA
142	<b>Z</b> 5	428	Cagtaggtggcgtcgccagggccttggcgcatggcgtcagggcccttggaggacggaatcaa
141	<b>Z1</b>	428	CtGTgGGTGGCGTCGCCAGGGCCCTGGCGCATGGCGTCAGGGCCGTGGAGGACGGAATLAA
139-145	consensus		CcGTgGGtGGCGTCGCCAGgGCccTgGCgCATGGcGTcAGGgctgTGGAGGACGGgaTcAA
			i j j i i i i i i j j i i i i i i i i i
			·
SEO ID NO			
145	DK13	489	TTATGCAACAGGGAATCTTCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCACTgCTCTCG
143	<b>Z</b> 6	489	TTATGCAACAGGGAATCTTCCCGGTTGCTCTTTCTCTATCTTCCTCTTGGCACTTCTTTCG
144	<b>Z</b> 7	489	TTATGCAACAGGGAACCTTCCCGGTTGCTCTTTLTCTATCTTCCTCTTGGCACTTCTTTCG
140	<b>Z8</b>	489	CTATGCAACAGGGAACCTTCCtGGTTGCTCTTTCTCTATCTTCCTCTTGGCACTTCTCTCG
139	Z4	489	CTATGCAACAGGGAATCTTCCGGGTTGCTCTTTCTCTATCTTCCTtTTGGCACTTCTtTCG
142	<b>Z</b> 5	489	CTATGCAACAGGGAATCTTCCTGGTTGCTCCTTtTCTATCTTCCTaCTTGCACTTtTCTCG
141	Z1	489	CTACGCAACAGGGAACCTTCCTGGTTGCTCLTTCTCTATCTTLCTTCTTGCACTTCTCTCG
<del>-</del>		203	CIACOLACOGRACETTCCIGGITGCTCETTCTCTCTTCTTCTCTCG
139-145	consensus		CTA+GCAACAGGAA+CTTCCCCCTTCCTC+TTCTCTTATCTTA
			CTALGCAACAGGGAALCTTCCCGGTTGCTCLTTCTCTATCTTCCTCLTGGCACTLCTCTCG
SEO ID NO	: ISOLATE		
145	DK13	550	TGCCTgACTGTTCCCgCtTCGGCC
143	Z6	550	TOCCHARTEROOLOGIC
144	26 27	550	TGCCTaACTGTTCCCaCCTCGGCC
140	27 28	220	TGCCTgACTGTTCCCGCCTCGGCC
		550	TGCCTaACcGTcCCAGCGTCtGCT
139	Z4	550	TGCCTcACtGTtCCAGCGTCgGCT
142	<b>Z</b> 5	550	TGCETGACAACACCgGCATCcGCT
141	Zl	550	TGCcTGACAACACCaGCATCtGCc
120 145			
139-145	consensus		TGCcTgACtgttCC-gC-TCgGCc

## FIGURE 61

SEO ID NO:	ISOLATE		
153	SA11	1 2	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCGCCGCCCACAGG
152	SA6	1 2	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCCAAAGAAACACCAACCGCCGCCCACAGG
146	SA4	1 2	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCCAAAGAAACACCAACCGCCGCCCACAGG ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCCACAGG
147	SA5	1 7	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAGAAACACCAACCGCCGCCCACAGG
148	SA7	1 2	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAGAAACACCAACCGCCGCCCACAGG
149	SAI	1 2	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAGAAACACCAACCGCCGCCCACAGG
150	SA3	1 7	ATGASTACGARTCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCECGCCCACAGG
151	SA13	7 7	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCCACAGG
131	SALS		ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAAAGAAACACCAACCGCCGCCCACAGG
146-153	consensus	A	TGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCgCCGCCCACAGG
SEO ID NO:	ISOLATE		
153	SA11	62	ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
152	SA6	62	ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGGTTTACTTGTTGCCGCGCAGGGG
146	SA4	62	ACGTLAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGGTTACTTGTTGCCGCGCAGGGG
147	SA5	62	ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGGTTTACTTGTTGCCGCGCAGGGG
148	SA7	62	A COTTA NOTTO COCCOCCOCCOCCA CARROLL CONTROLL ONTROLL CONTROL CONT
149	SAI	62	ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
150	SA3	62	ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
151	SA13	62	ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
131	SAIS	62	ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCGCGCAGGGG
146-153	consensus		ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTLTACTTGTTGCCGCGCAGGGG
SEO ID NO:	<u>ISOLATE</u>		
153	SA11	123	CCCTaGgtTGGGTGTGCGCGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
152	SA6	123	CCCTcGtaTGGGTGTGCGCGCGACTCGGAAGACTTCGGAACGGTCGCAACCCCGTGGaCGC
146	SA4	123	CCCTAGGTTGGGTGTGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
147	SA5	123	CCCTAGATTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
148	SA7	123	CCCTAGGTTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGGCGG
149	SA1	123	CCCCAGGTTGGGTGTGCGCGCGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGGCGG
150	SA3	123	CCCCAGGTTGGGTGTGCGCGCGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG
151	SA13	123	CCCLAGGTTGGGTGTGCGCAACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGACGG
146-153 c	Onconcue		
140-133	consensus		CCCtaGgtTGGGTGTGCGCGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGGCGG
SEO ID NO:	ISOLATE		
153	SA11	104	CCTC) CCCTC TO CCCC A CCCCC
152	SA11	104	CGTCAGCCTATTCCCAAGGCGCGCCAACCCACGGGCCGGTCCTGGGGTCAACCCGGGTACC
146	SA4	104	CGTCAGCCTATTCCCAAGGCGCGCCAAtCCGCGGGtCGGTCCTGGGGTCAACCCGGGTACC
147	SA5	104	CGCCAGCCTATTCCCAAGGCGCGCCAACCCACGGGCCGGTCCTGGGGTCAACCCGGGTACC
148		184	CGCCAGCCTATTCCCAAGGCGCGCCAACCCACGGGCCGGTCCTGGGGTCAACCCGGGTACC
149	SA7	184	CGCCAGCCTATTCCCAAGGCGCGCCAACCCACGGGCCGGTCCTGGGGTCAACCCGGGTACC
	SA1	184	CGCCAGCCTATTCCCAAGGCGCGCCAACCCACGGGCCGGTCCTGGGGTCAACCCGGGTACC
150	SA3	184	CGCCAGCCTATTCCCAAGGCtCGCCAGCCCACGGGCCGGTCCTGGGGTCAACCCGGTaCC
151	SA13	184	CGtCAGCCTATeCCCAAGGCGCCCAGCCCACGGGCCGGTCCTGGGGTCAACCCGGGTACC
146-153 c	onsensus		CGeCAGCCTATtCCCAAGGCgCGCCAaeCCaCGGGeCGGTCCTGGGGTCAACCCGGGTACC
CEO TO NO	T.C.O.T. N		
SEO ID NO:	ISOLATE	_ =	
153	SA11	245	CTTGGCCCtTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGCTGCTCTCCCCtCGAGG
152	SA6	245	CTIGGCCCTITACGCCAATGAGGGCCTCGGGTGGGTGGTTGCTCTCCCCCGACG
146	SA4	245	CTIGGCCCTITACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCCACG
147	SA5	245	CITGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCACC
148	SA7	245	CFIGGCCCTITACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGTTGCTCTCCCCCAGG
149	SAl	245	CTIGGCCCCTTACGCCAATGAGGGCCTCGGGTGGGCAGCGTGGTTGCTCTCCCCCGAGG
150	SA3	245	CTTGGCCCTTTACGCCAATGAGGGCCTCGaGTGGGCAGGGTGGTTGCTCTCCCCCGAGG
151	SA13	245	CTTGGCCCCTTTAtGCCAATGAGGGCCTCGGGTGGCAGGGTGGTTGCTCTCCCCCCGAGG
146-153 c	onsensus		CTTGGCCCcTTTAcGCCAATGAGGGCCTCGGGTGGCAGGGTGGTTGCTCTCCCCCCGAGG

#### FIGURE 61

SEO ID N	O: ISOLATE		
153	SA11	306	CTCTCGGCCTAACTGGGGCCCCAATGACCCCCGGCGAAGATCGCGCAATTTGGGCAAGGTC
152	SA6	306	CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
146	SA4	306	CTCTCCCCTA ATTCCCCCCCA TOACCCCCGGGAAAAT CGCGCAATTTGGGTAAGGTC
147		300	CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAGTCGCGCAATTTGGGTAAGGTC
	SA5	. 306	CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAATCGCGCAATTTGGGTAAGGTC
148	SA7	306	CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGAAAGTCGCGCAATTTGGGTAAGGTC
149	SA1	306	CTCTCGGCCTAATTGGGGCCCCAATGACCCCCGGCGGAAGTCGCGCAATTTGGGTAACGTC
150	SA3	306	CTCTCGGCCTAgTTGGGGCCCCAAcGACCCCCGGCGGAAATCGCGCAATTTGGGTAAGGTC
151	SA13	306	CTCTCGGCCTAaTTGGGGCCCCAAtGACCCCCGGCGGAAATCGCGCAACTTGGGTAAGGTC
146-153	consensus		CTCTCGGCCTAatTGGGGCCCCAAtGACCCCCGGCGaAaaTCGCGCAAtTTGGGtAAGGTC
			C1C1CGGCC1AAC1GGGCCCCAACGACCCCCGGCGAAATTGGGCAAGGTC
CDO TD 33			
SEO ID N			
153	SA11	367	ATCGATACCCTAACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
152	SA6	367	ATCGATACCCTAACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
146	SA4	367	ATCGATACCCTAACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
147	SAS	367	ATCGATACCCTAACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
148	SA7	367	ATCATACCTARCOTOCOGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
		36/	ATCGACACCCTAACATGCGGATTCGCCGACCTCATGGGGGTACATCCCGCTCGTAGGCGGCC
149	SA1	367	ATCGATACCCTAACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
150	SA3	367	ATCGATACCCTAACGTGCGGATTCGCCGAtCTCATGGGGGTACATCCCGCTCGTAGGCGGCC
151	SA13	367	ATCGATACCCTGACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
146-153	consensus		ATCGA+ACCCT+ACCTCCATTCCCCCATTCCCCCATCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCATCCCCCC
			ATCGAŁACCCT&ACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC
CDO TD W			
SEO ID NO			
153	SA11	428	CCGTTGGGGGCGTCGCAAGGGCCCTCGCACACGGTGTGAGGACCTCTTGAGGACGGGGTAAA
152	SA6	428	CCGTTGGGGGCGTCGCAAGGGCtCTCGCACACGGTGTGAGGGTTCTTGAGGACGGGGTAAA
146	SA4	428	CCGTTGGGGGCGTCGCAAGGGCCCTtGCACATGGTGTGAGGGTTCTTGAGGACGGGGTAAA
147	SA5	428	CCCTTCCCC ACCCCCCCA ACCCCCA A TOTAL CONTROL OF THE ACCCCCCCA ACCCCCA ACCCCCA ACCCCCA ACCCCCA ACCCCCA ACCCCCA ACCCCCA ACCCCCA ACCCCCA ACCCCA ACCCA ACCCCA ACCCA ACCCCA ACCCA ACCA ACCCA ACCCA ACCCA ACCA ACCA ACCA ACCA ACCA ACCA
148	SA7	420	CCGTTGGGGGCGTCGCAAGGGCCCTCGCACATGGTGTGAGGGTTCTTGAGGACGGGGTAAA
		428	CCGTTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTTCTTGAGGACGGGGTAAA
149	SA1	428	CCGTTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTTCTTGAGGACGGGGTAAA
150	SA3	428	CCGTTGGGGGCGTCGCAAGGGCTCTCGCACAtGGTGTGAGGGTTCTTGAGGACGCGTAAA
151	SA13	428	CCGTTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTCCTTGAGGACGGGGTAAA
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
146-153	consensus		CCGTTGGGGGCGTCGCAAGGGC+CTCCCACACACGCTCACACACACACACACACACACACACA
			CCGTTGGGGGCGTCGCAAGGGCtCTcGCACAcGGTGTGAGGGGCTCGGGGGTAAA
SEO ID NO	. TOOL SEE		
153	SA11	489	tTATGCAACAGGGAATcTtCCCGGTTGCTCTTTCTCCATCTTTaTCCTTGCACTTCTCTCG
152	SA6	489	CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTTTTCTCTGCACTTCTCTCG
146	SA4	489	CTATGCAACGGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
147	SA5	489	CTATGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
148	SA7		TREGERAL AND COCCUMENTATION OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE C
149	SA1	400	tTACGCAACAGGGAATCTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTCTCG
		489	CTACGCAACAGGGAATTTGCCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCC
150	SA3	489	CTACGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
151	SA13	489	CTAEGCAACAGGGAATTTACCCGGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCA
146-153	consensus		cTAtGCAACaGGGAATtTgCCCGGTTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTCTCq
			and the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t
SEO ID NO	: ISOLATE		
153			MCC+M-1 C00MC00
	SA11	550	TGCtTgACCGTCCCgGCCaCTGCA
152	SA6	550	TGCCTAACCGTCCCEGCCTCTGCA
146	SA4	550	TGCCTGACCGTCCCgGCCTCTGCA
147	SA5	550	TGCETGACCGTCCCAGCCTCTGCA
148	SA7	550	TGCCTGACCGTCCCAGCCTCcGCA
149	SA1	550	TGECTGAECATCCCGGCCTCTGCA
150	SA3	550	TOCATOR COMPANY COMPANY
		550	TGCCTGACCGTCCCGGCCTCTGCA
151	SA13	550	TGCCTGACtGTCCCGaCCTCTGCc
146-153	consensus		TGccTgAccgTCCCggCCtCtGCa

## FIGURE 6J

SEO ID NO	: Genotype		
103-154	cons.	1 .	ATGAGCACgaaTCCtAAACCtCAAAGAaAaACCaaAcGtAAcACcAaCCgcCGCCCacagG
103-124	1	1 .	ATGAGCACGAATCCTAAACCTCAAAGAAAACCAAACGTAACACCAACCGcCGCCCACAGG
125-134	2	1 .	ATGAGCACAAATCCtAAACCtCAAAGAAAAACCAAAAGAAACACAAACCGcCGCCCACaca
135-138	3	1 .	ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAAGAAACACCATCCGTCGCCCACAGG
139-145	4	1 .	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCAAACGTAACACCAACCGCCGCCCCCATGG
146-153	5	1 .	ATGAGCACGAATCCTAAACCTCAAAGAAAAACCaAAAGAAACACCAACCaCCGCCCACAGG
154	6	1 /	ATGAGCACACTTCCAAAACCCCAAAGAAAACCAAAGAAACACCCAACCGTCGCCCAACGG
SEO ID NO	: Genotype		
103-154	cons.	62	AcgTcAAgTTcCCgGGcGGtGGtCAGATCGTtGGtGGAGTtTActTGtTGCCGCGCAGGGG
			negrous graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Graduate Grad
103-124	1	62	ACGTCAAGTTCCCGGGCGGCGGCCAGATCGTLGGTGGAGTLTACCTGTTGCCGCGCAGGGG
125-134	2	62	ACGTEAAGTTCCCGGGCGGCGGCCAGATCGTTGGCGGAGTaTACTTGCTGCCGCGCAGGGG
135-138	3	62	ACGTCAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGG
139-145	4	62	ACGTAAAGTTCCCqGGtGGtGGcCAGATCGTTGGCGGAGTTTACTTG+TGCCGCACCCC
146-153	5	62	ACGTcAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTLTACTTGTTGCCGCGCAGGGG
154	6	62	ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGCGGAGTTTACTTGTTGCCGCGCAGGGG
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103-154	cons.	123	CCCaegatTeccatcatcatcatcatcatcatcatcatcatcatcatcat
	· · · · ·		CCCcaGgtTGGGTGTGCGCgCgaCtaGgAAgaCTTCcGAgCGgTCgCAaCCtcGtGGaaGg
103-124	1	123	CCCcaGgTTGGGTGTGCGCGCgaCtAGGAAGACTTCcGAGCGgTCgCAACCTCGtGGaaGg
125-134	2	123	CCCCAGGTTGGGTGTGCGCGCGACaAGGAAgaCTTCcGAgCGaTCCCAGCCGCGCGAGG
135-138	3	123	CCCACGATTGGGTGTGCGCGCGACGCGTAAAACTTCTGAACGGTCaCAGCCGACGA
139-145	4	123	CCCcaGgTTGGGTGTGCGCqCqaCTcGqAAGACTTCGGAGCGGTCqCAACCTCG+CGcAGq
146-153	5	123	CCCtaGgtTGGGTGTGCGCGCqACTCGGAAGACTTCaGAACGGTCGCAACCCCCCCCCCCCC
154	6	123	CCCCCGGTTGGGTGTGCGCGCGACGAGAAAGACTTCCGAGCGATCCCAGCCCAGAGGCAGG
SEO ID NO:	Genotime		
103-154	cons.	184	CGAC DGCCC DTGCCCC DGCGCCCCCCCCCCCCCCCCCCCC
			CGaCAgCCtATcCCcaAgGctCGcCggcccgagGGcaggtcCTGGGctcagCCcGGgtAcC
103-124	1	184	CGaCAaCCTATCCCCAAGGCtCGcCggCCCGAGGGcAGGgCCTGGGCtCAGCCcGGGtAcC
125-134	2	184	CGCCAGCCCATCCCGAAAGATCGGCGCtCCACtGGCAAGtCCTGGGGAAaaCCaGGATAtC
135-138	3	184	CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCCGGTCCTGGGCTCAGCCAGC
139-145	4	184	CGtCAgCCTATCCCCaAGGCaCGtCggtccGAGGGcAGgTCCTGGGCtCAgCCcGcgtacC
146-153	5	184	CGCCAGCCTATtCCCAAGGCqCGCCAacCcaCGGGcCGGTCCTGGGGTCAacCcGcTacC
154	6	184	CGCCAACCTATACCAAAGGCGCGCCAGCCCCAGGGCAGGCA
SEO ID NO:	Genotime		
103-154	cons.	245	CtTGGCCCTTTAtGacaatcAcattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccattaccat
			CtTGGCCccTcTAtGgcaAtGAgGGcttcGggTGGGCaGGaTGGcTccTgTCcCCcCgcGG
103-124	1		
125-134	_	245	CtTGGCCCTCTAtGgCaAtGAGGGCttgGGGTGGGCaGGATGGCTCCTCTCAGGCAGG
135-138	2	245 245	CtTGGCCCTCTAtGgCaAtGAGGGCttgGGTGGGCaGGATGGCTCCTGTCaCCCCgtGG CtTGGCCCTgTAtGGgAAtGAGGGCctCGGCTGGGCAGGTTGGCTCCTGTTCGCGGGG
			CTIGGCCCTGTAtGGgAAtGAGGGcctCGGcTGGGCaGGtTGGCTCCTGTCCCCCCG
139-145	2 3 4	245	CETGGCCCTGTAEGGAAEGAGGGCCECGGGTGGGCAGGETGGCTCCTGTCCCCCGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CETGGCCECTETACGGCAAEGAGGGTGGGCTGGGTGGCTCCTGTCCCCCCGCGG
146-153	2 3 4 5	245 245 245 245	CTTGGCCCTTTAEGGAAEGAGGGCCECGGCTGGGCAGGETGGCTCCTGTCCCCCGGGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CtTGGCCCTTTACGGCAAEGAGGGCTGCGGGTGGGTGGTTGCTCCCCCCGGGG CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGETGCTCTCCCCACGACG
	2 3 4	245 245 245	CTTGGCCCTTTAEGGAAEGAGGGCCECGGCTGGGCAGGETGGCTCCTGTCCCCCGGGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CtTGGCCCTTTACGGCAAEGAGGGCTGCGGTGGGCAGGGTGGETGCTCTCCCCCGCGG CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGETGCTCTCCCCCGAGG
146-153 154	2 3 4 5 6	245 245 245 245	CETGGCCCTGTAEGGAAEGAGGGCCECGGGTGGGCAGGETGGCTCCTGTCCCCCGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CETGGCCECTETACGGCAAEGAGGGTGGGCTGGGTGGCTCCTGTCCCCCCGCGG
146-153 154 SEO ID NO:	2 3 4 5 6	245 245 245 245 245	CTTGGCCCTGTAEGGAAEGAGGCCECGGCTGGCAGGETGGCTCCTGTCCCCCGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGCAGGGTGGCTCCTGTCCCCACGCGG CTTGGCCECTETACGGCAAEGAGGGCTGCGGTGGGCAGGGTGGCTCCTGTCCCCCCGAGG CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGCAGGTTGGCTCCTCTCCCCCCGAGG CTTGGCCTCTTTATGGAAACGAGGGCTGTGGGTGGGCAGGTTGGCTCCTCTCCCCCGCGG
146-153 154	2 3 4 5 6	245 245 245 245	CTTGGCCCTTTAEGGAAEGAGGGCCECGGCTGGGCAGGETGGCTCCTGTCCCCCGGGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGGTGGGCAGGGTGGCTCCTGTCCCCACGCGG CtTGGCCCTTTACGGCAAEGAGGGCTGCGGGTGGGTGGTTGCTCCCCCCGGGG CTTGGCCCCTTTACGCCAATGAGGGCCTCGGGTGGGCAGGGTGGETGCTCTCCCCACGACG
146-153 154 SEO ID NO:	2 3 4 5 6 Genotype cons.	245 245 245 245 245 245	CTTCcggCCtagtTGGGGcCccActGAcCCCCGGCgtaggTCgCGcAAttTGGGtAagGTC
146-153 154 <u>SEO ID NO:</u> 103-153	2 3 4 5 6	245 245 245 245 245	CTTCCGGCCTATTAGGGAATGAGGCCCCAGGGCTGGCTGG
146-153 154 <u>SEO ID NO:</u> 103-153 103-124	2 3 4 5 6 <u>Genotype</u> cons.	245 245 245 245 245 245 306	CTTGCCCCTGTAEGGAAEGAGGCCCCACEGACCCCCGGCGLAGGTCGCTAATCTGGCAAGGCCCCCGCGGCCTTGGCCCCTTTACGTAACGAGGGCTGCGGTGGCAGGTGGCTCCTGTCCCCACGCGGCCTTGGCCCCTTTACGCAATGAGGGCTGCGGTGGCAGGTGGCTCCTGTCCCCCCGGGGCTTGGCCCTTTACGCCAATGAGGGCCTCTGGGTGGCAGGTTGGCTCCTCTCCCCCCGGGGCTTGGCCTCTTTATGGAAACGAGGGCTGTGGTGGCAGGTTGGCTCCTGTCCCCCCGCGGCCCCCCGCGGCCCCCGGCGCCCCCC
146-153 154 SEO ID NO: 103-153 103-124 125-134 135-138 139-145	2 3 4 5 6 <u>Genotype</u> cons.	245 245 245 245 245 245 306 306	CTTCCGCCTGTAEGGAATGAGGCCCCACTGGCTGGCAGGTTGGCTCCTGTCCCCCGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGTGGCAGGTTGGCTCCTGTCCCCACGCGG CTTGGCCCTCTTACGCAATGAGGGCTGCGGTGGCAGGTTGGCTCCTGTCCCCCCGCGG CTTGGCCCTTTACGCCAATGAGGGCCTCGGGTGGCAGGTTGGCTCCTCCCCCCGAGG CTTGGCCTCTTTATGGAAACGAGGGCTGTGGGTGGCAGGTTGGCTCCTGTCCCCCCGCGG  cTCtcggCCtagtTGGGGcccActGAcCCCCGGCgtaggTCgCGcAAttTGGGtAagGTC cTCtCGGCCTAgtTGGGCCCActGACCCCCGGCGtAGGTCGCGCAATtTGGGTAAGGTC tTCtCgtCCttctTGGGGCCCCActGACCCCCGGCGAAGTCCGCAATTTGGGTAAGGTC CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGAAGGTCCCGCAATTTTCGGTAAACGTC
146-153 154 SEO ID NO: 103-153 103-124 125-134 135-138 139-145 146-153	2 3 4 5 6 <u>Genotype</u> cons.	245 245 245 245 245 306 306 306 306 306 306	CTTGGCCCTGTAEGGAATGAGGGCCCCGGCGGGTGGCAGGTTGGCTCCTGTCCCCCGGGGCTTGGCCCCTTTATGGTAACGAGGGCTGCGGTGGCAGGGTGGCTCCTGTCCCCCCGCGGGCTTGGCCCCTTTACGCAATGAGGGCTGCGGTGGCAGGTTGGCTCCTGTCCCCCCGGGGCTTGGCCCCTTTACGCCAATGAGGGCCTCGGTTGGCAGGTTGGCTCCTGTCCCCCCGGGGCTTGGCCTCTTTATGGAAACGAGGGCTGTGGTGGGCAGGTTGGCTCCTGTCCCCCCGGGGCTTGGCCTCTTTATGGAAACGAGGGCCCCCGGCGTAGGTCGCCAAATTTGGGTAAGGTCCTCCGGCCTAGTTGGGCCCAAAGGACCCCCGGCGTAGGTCGCGAAATTTGGGTAAGGTCCTCCGTCCATCTTGGGGCCCAAACGACCCCCGGCGAAGTCCCGCAATTTGGGTAAAGTCCTCCGGCCGCGCTCCTTTTGGGGCCCAAACGACCCCCGGCGAAGTCCCGCAATTTGGGTAAAGTCCTCCGGCCGCTCTTTTGGGCCCAAATGATCCCCGGCGAAGTCCCGCAATTTGGGTAAGGTCCTCCGGCCTAATTGGGCCCAAACGACCCCCGGCGAAGTCCCGCAATTTGGGTAAAGTCCTCCGGCCTAATTGGGCCCAAACGACCCCCGGCGAAGTCCCGCCAATTTGGGTAAAGTCCTCCGGCCTAATTGGGCCCAAATGATCCCCGGCGAAATTTGCGCAATTTTAGGTAAAGTCCTCTCGGCCTAATTGGGTAAAGTCCCCCGGCGAAATTTTAGGTAAAGTCCCTCCGGCCTAATTTAGGTAAAGTCCCTCCGGCCTAATTTAGGTAAAGTCCCTCCGGCCTAATTTAGGTAAAGTCCCTCCGGCCTAATTTAGGTAAAGTCCCTCCGGCCGAAATTTAGGTAAAGTCCCTCTCGGCCTAATTTAGGTAAAGTCCCTCCGGCCGAAATTTTAGGTAAAGTCCCTCCGGCCGAAATTTTAGGTAAAGTCCCTCTCTCGGCCTAATTTAGGTAAAGTCCCTCCGGCCGAAATTTTAGGTAAAGTCCCTCTCTCGGCCTAATTTAGGTAAAGTCCCTCTCTCGGCCTAATTTAGGTAAAGTCCCTCTCTCGGCCTAATTTAGGTAAAGTCCCTCTCTCGCCTAATTTAGGTAAAGTCCCTCTCTCT
146-153 154 SEO ID NO: 103-153 103-124 125-134 135-138 139-145	2 3 4 5 6 <u>Genotype</u> cons.	245 245 245 245 245 306 306 306 306 306	CTTCCGCCTGTAEGGAATGAGGCCCCACTGGCTGGCAGGTTGGCTCCTGTCCCCCGCGG CTTGGCCCCTCTATGGTAACGAGGGCTGCGGTGGCAGGTTGGCTCCTGTCCCCACGCGG CTTGGCCCTCTTACGCAATGAGGGCTGCGGTGGCAGGTTGGCTCCTGTCCCCCCGCGG CTTGGCCCTTTACGCCAATGAGGGCCTCGGGTGGCAGGTTGGCTCCTCCCCCCGAGG CTTGGCCTCTTTATGGAAACGAGGGCTGTGGGTGGCAGGTTGGCTCCTGTCCCCCCGCGG  cTCtcggCCtagtTGGGGcccActGAcCCCCGGCgtaggTCgCGcAAttTGGGtAagGTC cTCtCGGCCTAgtTGGGCCCActGACCCCCGGCGtAGGTCGCGCAATtTGGGTAAGGTC tTCtCgtCCttctTGGGGCCCCActGACCCCCGGCGAAGTCCGCAATTTGGGTAAGGTC CTCCCGTCCATCTTGGGGCCCCAAACGACCCCCGGCGAAGGTCCCGCAATTTTCGGTAAACGTC

### FIGURE 6J

SEO TO	NO: Genotype		<b>7</b> /2
103-154		367	ATCCAT ACCOTA COTTO COTTO COTTO COCO A COMO ACCO COMO ACCO COMO COMO ACCO ACC
103-13-	comb.	307	ATCGALACccTcACgTGcgGctTcGCCGAcCTCATGGGgTACaTcCCgcTCGTcGGcGccC
103-124	1	367	ATCGALACCCTCACaTGCGGCTTcGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGCCC
125-134	-	367	ATCGALACCCTAACGTGCGGCLTTGCCGACCTCATGGGGTACATCCCCGTCGTCGGCGCCC
135-138		367	ATCGATACCCTLACGTGCGGaTTCGCCGACCTCATGGGGTACATCCCGGTCGTCGGCGCTC
139-145		367	ATCGATACCCTGACGTGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
146-153	-	367.	ATCGATACCCTTACGTCCGCATTCCCCCACCTCGTACGCCCCCCCC
154	6	367	ATCGALACCTAACGTGCGGATTCGCCGACCTCATGGGGTACATCCCGCTCGTAGGCGGCC ATCGATACCCTAACGTGTGGGTTCGCCGATCTCATGGGGTACATTCCCGTCGTGGGCGCGC
131	•	367	ATCGATACCTAACGTGTGGGTTCGCCGATCTCATGGGGTACATTCCCGTCGTGGGCGCGC
SEO ID	NO: Genotype		
103-154		428	CcgTaGGgGGcGtcGCcaggGCccTgGCgCAtGGcGTcaGggttcTgGAgGACGGggTgAA
103-124	1	428	CccTaGGgGGcGcTGCCAGgGCccTGGCgCAtGGcGTCCGgGTtcTGGAgGACGGCGTGAA
125-134	2	428	CggTtGGaGGcGTcGCCAGAGCtCTgGCaCAtGGtGTgAGgGTcCTGGAgGACGGgaTaAA
135-138	3	428	CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
139-145	4	428	CcGTgGGtGGCGTCGCCAGgGCccTgGCgCaTGGcGTcAGGgctgTGGAGGACGGgaTcAA
146-153	5	428	CCGTTGGGGGCGTCGCAAGGGCtCTcGCACAcGGTGTGAGGGCtCTTGAGGACGGGGTAAA
154	6	428	CTTTGGGCGGCGTCGCGCTCGCACATGGCGTGAGGGCAATCGAGGACGGGATCAA
			The state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the s
SEQ ID			·
103-154	cons.	489	cTatGCAACaGGgAAttTgCCcGGTTGCtCtTTcTCtATcTTccTccTgGCtcTgcTgTCc
103-124	1	489	CTALGCAACAGGGAALCTGCCCGGTTGCLCLTTCTCTATCTTCCTCLTGGCLLTGCTGTCC
125-134	2	489	tTAtGCAACaGGqAAttTqCCtGGTTGCTCtTTtTCTATCTTctTqCTtGCcCTtcTCTCC
135-138	3	489	TTTCGCAACAGGGAACTTGCCCGGTTGCTCCTTTTCTATCTTCCTTC
139-145	4	489	CTALGCAACAGGGAALCTTCCCGGTTGCTCLTTCTCTATCTTCCTCLTGGCACTLCTCTCG
146-153	5	489	CTAtGCAACAGGGAATtTGCCCGGTTGCTCTTTCTCtATCTTTaTCCTTGCACTTCTCTCG
154	6	489	TTATGCAACAGGGAATCTCCCCGGTTGCTCTTTCTCTATCTTCCTTTTGGCACTACTCTCG
	NO: Genotype		
103-154	cons.	550	TGcctgaccgtcCCagcttCtgct
102 124	_		
103-124	1	550	TGttTgACcatcCCaGctTCcGCt
125-134	2	550	TGCatCaCagtgCCaGtgTCtGCt
135-138	3	550	TGCtTAaTTCATCCaGCAGCTAGT
139-145	4	550	TGCcTgACtgttCCagCgTCgGCc
146-153	5	550	TGccTgAccgTCCCggCCtCtGCa
154	6	550	TGCCTCACAACGCCAGCTTCGGCT

# FIGURE 6K

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# FIGURE 6K

MttfGGtAagGtCATCGAtACccTcACgGCGTCCCGACCTCGTCGGCGCCCCCgTaGGGGCGtCCCggGCGCTCGTCGGCGCCCCCgTaGGGGCGtCCCggGCGCTGCGGCCCCGTGCGCGCCCCGTGCGCCCGGTGCCTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCGCCCTGCCTGCCTGCCTGCCTGCTCTCTTTTTT	187   480   490   500   510   520   530   540   550   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570   570
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370 GICALGALA	CCGG9919AA
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750 CGCAAtt	6cGTca6ggttcTgGAgGACG 
Genotype 1/1a 11/1b 11/2b 1V/2b 2c (V)/3a 4b 4c 4c 4d 4d 6a	Genotype 1/18 11/1b 11/2b 2c (V)/3a 4b 4c 4c 4d 4d 4f 4e 6a
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## FIGURE 7A

SEO ID NO: ISOLA	TE
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	A MOINFRPUKKIRKNINKRPUDVKFPGGGOTVGGVYLLDDDGDDIGVDATDVTGCDDGDDCD
155 I	K7 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRAPRKTSERSQPRGR
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156 US	62 ROPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
157 S	62 ROPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
	- 0
	NE 04 KUPIPKAKKPEGKIWAUPGIPWPLIGNEGCGWAGWIISPRGSPDSWGDTDDDDDDDDDDXXX
155 D	K7 62 ROPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
155-160 consens	RQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
SEO ID NO: ISOLA	
156 US	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
157 S	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
158 S	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
133	(7 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
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#### FIGURE 7B

SEO ID NO:	ISOLATE	
175	P8	1 MSTtPKPQRKTKRNTsRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
170 162	·IND8 S45	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVRATRKTSEDSÖDDGD
171	\$ <del>\$</del> 5	<ul> <li>MSTNPKPÖRGTKRNTNRRPÖDVKFPGGGÖTVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR</li> <li>MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖTVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR</li> </ul>
163	Ďĺ	1 MSTNPKPORKTKRNTNRRPODVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
165	P10	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVPATPKTCFPCOPPGP
169	IND3	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVRATPKTGEPGÖDDGD
164 166	US6 DK1	1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖIVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR 1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖIVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
167	T10	1 MSTNPKPORKTKRNTNRRPODVKFPGGGÖIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
168	SW2	1 MSTNPKPQRKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATPKTGEPGÖDDGD
161 174	SA10 HK4	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVPATPKTGFPGÖDDGD
172	HK3	1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR 1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
176	T3	I MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVPATPKTGEPGÖDDGD
173	HK5	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
		,
161-176	consensus	MSTnPKPQRkTKRNTnRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
		1 ?
SEO ID NO:	ISOLATE P8	62 ROPIPKARRPEGRAWAOPGHPWPI.YaNEGI.GWAGWI.I.SDBCSBBSWGDTDDDDDDDDDDD
170	IND8	62 ROPIPKARRPEGRAWAOPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV 62 ROPIPKARRPEGRAWAOPGHPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
162	S45	02 KOPIPKAKKPEGKAWAOPGHPWPLYGNEGLGWAGWILSPRGSRPSWGDTDDDDDDDDDDCDNT CKT/
171 163	S <del>9</del>	~ 62 KQP1PKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPADPDDDDDDDDDXTGKT
165	D1 P10	62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV 62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
169	IND3	62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV 62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
164	US6	92 KOPIPKAKRPEGRAWAOPGYPWPLYGNEGMGWAGWII.SPRGSRDSWGDTDDDDDDDDDDDCDNT GV7
166 167	DK1 T10	62 KQPIPKARRPEGRAWAOPGYPWPLYGNEGMGWAGWII.SPRGSPDSWGDnDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
168	SW2	62 RÖPIPKAROPEGRAWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNIGKV 62 RÖPIPKAROPEGRAWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNIGKV
161	SA10	62 KQPIPKARQPEGRTWAOPGYPWPLYGNEGIGWAGWLLSPRGSRPSWGDTDDDDDDDDDDCDNT GYTI
174 172	HK4	62 KQP1PKARQPEGRTWAQPGYPWPLYGNEGMGWAGWLLSPRGSRDSWGDTDDDDDDDDDDCDNT GYTI
176	НКЗ Т3	62 ROPIPKAROPEGRTWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV 62 ROPIPKARRPEGRAWAOPGYPWPLYGDEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
173	HK5	62 RÖPIPKARRPEGRAWAÖPGYPWPLYGDEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV 62 RÖPIPKARRPEGREWAÖPGYPWPLYGNEGMGWAGWLLSPNGSRPSWGPTDPRRRSRNLGKV
•		, See a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see a see
161-176	consensus	RQPIPKARrPEGRaWAQPGyPWPLYgnEG-GWAGWLLSPrGSRPsWGPtDPRRRSRNLGKV
SEO ID NO:	<b>ISOLATE</b>	
175 170	P8 IND8	123 IDTLTCGFADLMGYIPLVGgPLGGVARALAHGVRVvEDGVNYATGNLPGCSFSIFLLALLS
162	S45	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
171	S9	123 IDTLICGFADLMGYIPLVGAPLGGAARALAHGVRVI.FDGVNVATGNI.DGCCCCCTTIIATIC
163 165	D1	123 IDILICGEADLEGGIPLOGAPLGGAARALAHGVRVI.EDGVNVATGNI.DGCGEGTEITATTG
169	P10 IND3	123 IDILICGFADLMGYIPLVGAPLGGAARALAHGVRVT.RDGVNVATGNT.DGCCECTET.T AT T C
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
166	DK1	123 IDILICGEADLMGXIPLVGAPLGGAARALAHGVRVT.EDGVNVATGNT.DGCGGGGGGTGTTXTTG
167 168	T10 SW2	143 IUILICGFADLMGYIPLVGAPLGGAARAT.AHGVDVT.FDGINIVATGNT.DGCCCCCTCTTATT.C
161	SAIO	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCPFSIFLLALLS
174	HK4	143 LULLICUFAULMGI LPLVGAPIGGVARALANGVDVvEDGVNVATGNT DGCCCCCTCT T X T + C
172 176	HK3	143 IUTUTCGFADLMGYIPLVGAPIGGVARAT.AHGVDVITEDGVNVATGNI DGCCCCCTCT ATT C
173	T3 HK5	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNIPGCSFSIFLLALLS
161-176 c	consensus	IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRV1EDGVNYATGN1PGCsFSIFLLALLS
SEO ID NO:	<b>ISOLATE</b>	
175 170	P8	184 CLTipasa
162	IND8 S45	184 CLTVPASA 184 CLTIPASA
	0.5	-01 CHAIFMAN

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#### FIGURE 7B

171	S9	184	CLTIPASA
163	D1	184	CLTIPASA
165	P10	184	CLTIPASA
169	IND3	184	CLTIPASA
164	US6	184	CLTIPASA
166	DK1	184	CLTIPASA
167	T10	184	CLTIPASA
168	SW2	184	CLTIPASA
161	SA10	184	CLTIPASA
174	HK4	184	CLTIPASA
172	HK3	184	CLTtPASA
176	<b>T</b> 3	184	CLTiPASA
173	HK5	184	CLTtPvSA
161-176	COREARENE		CITIBERA

## FIGURE 7C

SEO ID NO:	ISOLATE	
173	HK5	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
176	T3	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVRATPKTSERSÕDDGD
172	HK3	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVRATRKTSERSÕDDGD
174	HK4	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
161 168	SA10 SW2	1 MSTNPKPORKTKRNTNRRPÖDVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
167	T10	1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖTVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR 1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖTVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
166	DK1	1 MSTNPKPORKTKRNTNRRPODVKFPGGGÖIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
164	US6	1 MSTNPKPORKTKRNTNRRPODVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
169	IND3	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSRRSADDGD
165	P10	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
163	D1	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVRATRKTSERSÖRRGR
156	US11	1 MSTNPKPQRKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
157	S14 SW1	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
158 159	S18	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
160	DR4	1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR 1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
155	DK7	1 MSTNPKPORKTKRNTNRRPODVKFPGGGÖLVGGVYLLPRRGPRLGVRAPRKTSERSOPRGR
170	IND8	1 MSTNPKPÖRKTKRNTNRRPÖDVKFPGGGÖLVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR
162	S45	1 MSTNPKPORGTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSRRSÖPRGP
171	S9	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSÖPPGP
175	P8	1 MSTtPKPQRKTKRNTsRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
155-176	consensus	MST DEDODETED DDDODIWED CCCOTTE CHALL ADDODDE COME.
133 170	COMBEMBUB	MSTnPKPQRkTKRNTnRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRA+RKTSERSQPRGR
000 TD 110		
SEO ID NO:		60 000000000000000000000000000000000000
173 176	HK5 T3	62 ROPIPKARRPEGREWAQPGYPWPLYGNEGMGWAGWLLSPHGSRPSWGPTDPRRRSRNLGKV
172	HK3	62 ROPIPKARRPEGRAWAOPGYPWPLYGdEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNLGKV
174	HK4	62 ROPIPKAROPEGRTWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPNWGPTDPRRRSRNIGKV 62 ROPIPKAROPEGRTWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNIGKV
161	SA10	62 ROPIPKAROPEGRTWAOPGYPWPLYGNEGIGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
168	SW2	62 ROPIPKAROPEGRAWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
167	<b>T10</b>	62 RQPIPKARQPEGRAWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPRRRSPNIGKV
166	DK1	62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPnDPDPDSDNT.CKV
164	US6	62 RQPIPKARRPEGRAWAOPGYPWPLYGNEGMGWAGWLLSPRGSRPSWGPTDPDPDPSDNT.GKV
169 165	IND3 P10	62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
163	D1	62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV 62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRBSRNLGKV
156	บราว	62 ROPIPKARRPEGRAWAOPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV 62 ROPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
157	S14	62 ROPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
158	SW1	62 ROPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
159	S18	62 RQPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRPRSRNTGKV
160	DR4	62 ROPIPKARRPEGRTWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRPRSPNT.GKV
155	DK7	62 RQPIPKARRPEGRTWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRRSRNIGKV
170 162	IND8	62 ROPIPKARRPEGRAWAOPGHPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV
171	S45 S9	62 ROPIPKARRPEGRAWAOPGHPWPLYGNEGLGWAGWLLSPRGSRPSWGPTDPRRRSRNLGKV 62 ROPIPKARhPEGRAWAOPGVPWPLYGNEGLGWAGWLLSPRGSRPSWGPDPRPRBSRNLGKV
175	P8	62 RÖPIPKARhPEGRAWAÖPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRRRSRNLGKV 62 RÖPIPKAR:PEGRAWAÖPGhPWPLYANEGLGWAGWLLSPRGSRPSWGPtDPRRRSRNLGKV
_		
155-176	consensus	RQPIPKARrPEGRaWAQPGyPWPLYgnEG-GWAGWLLSPrGSRP#WGPtDPRRRSRNLGKV
SEO ID NO:	<b>ISOLATE</b>	
173	HK5	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNYATGNiPGCSFSIFLLALLS
176	T3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLRDGVNYATGNI.DGCGFGTFI.I.A.I.I.G
172	нкз	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVI.FDGVMVATGNT.DGCGFGTFTT.XTT.G
174 · 161	HK4	123 IDTLTCGFADLMGYIPLVGAPIGGVARALAHGVRVvFDGVNVATGNT.DCCCCCTCTTT.ATT.C
168	SA10 SW2	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCPFSIFLLALLS
167	T10	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
166	DK1	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
169	IND3	123 IDTLTCGFADLMGYIPLVGAPIGGAARAT.AHGVDVT.EDGVNVATGNT.DGCCECTETTATTC
165	P10	123 IDTLTCGFADLMGYIPLVGAPIGGAARAI.AHGVPVI.EDGVNVATGNI.DGCGEGTEI i ki i c
163 156	D1	143 IDTLTCGFADLMGYIPLVGAPLGGAARAT.AHGVRVT.EDGVNVATGNT.DGCCCCCTCTTATTC
	US11	143 IDTLTCGFADLMGYIPLVGAPLGGAARATAHGVRVT.FDGVNVATGNT.DGCCCCCTCTTATTC
157	S14	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNIBGGSESIFLLALLS
		143 IDTLTCGFADLMGYIPLVGAPLGGAARATAHGVRVT.FDGVNVATGNT.DGCCCCCTCTTATTC

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155-176

consensus

#### FIGURE 7C

159 160 155 170 162 171 175	S18 DR4 DK7 IND8 S45 S9 P8	123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 124 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 125 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 126 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 127 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 128 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVVEDGVNYATGNLPGCSFSIFLLALLS 129 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVVEDGVNYATGNLPGCSFSIFLLALLS 120 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVVEDGVNYATGNLPGCSFSIFLLALLS
SEQ ID NO 173 176 172 174 161 168 167 166 169 165 163 157 158 159 160 157 170 162 171	D: ISOLATE  HK5  T3  HK3  HK4  SA10  SW2  T10  DK1  US6  IND3  P10  D1  US11  S14  SW1  S18  DR4  DK7  IND8  S45  S9  P8	184 CLTtPVSA 184 CLTtPASA 184 CLTIPASA 184 CLTVPASA

CLTiPaSA

#### FIGURE 7D

SEO ID NO:         ISOLATE           179         T9           178         US10           180         T2           177         T4	1 MSTNPKPORKTIRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSOPRGR 1 MSTNPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTIPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTnPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
177-180 consensus	${ t MST}_{ t D}{ t PKPQRKT}{ t kRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR$
SEQ ID NO:         ISOLATE           179         T9           178         US10           180         T2           177         T4           177-180         consensus	62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPSDPRHRSRNVGKV 62 ROPIPKDRRPTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPtDPRHRSRNVGKV 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV ROPIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
SEO ID NO:         ISOLATE           179         T9           178         US10           180         T2           177         T4           177-180         consensus	123 IDTLTCGFADLMGYIPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 123 IDTLTCGFADLMGYIPVVGAPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 124 IDTLTCB1ADLMGYvPVVGgPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS 125 IDTLTCGfADLMGYiPVVGaPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
SEO ID NO:         ISOLATE           179         T9           178         US10           180         T2           177         T4           177-180         consensus	184 CITtPASA 184 CITIPVSA 184 CITIPVSA 184 CITIPVSA CITIPVSA

#### FIGURE 7E

SEQ ID NO:         ISOLATE           183         DK11           184         SW3           181         T8           182         US1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRLTRKTSERSQPRGR 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR 1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
185 DK8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
181-185 consensus	MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSERSQPRGR
SEO ID NO:         ISOLATE           183         DK11           184         SW3           181         T8           182         US1           185         DK8	62 ROPIPKDRRSTGKDWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHKSRNLGKV 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
181-185 consensus	RQPIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGSrPtWGPTDPRHrSRNLGkV
SEO ID NO:         ISOLATE           183         DK11           184         SW3           181         T8           182         US1           185         DK8	123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS 123 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS 124 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS 125 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS 126 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS 127 IDTITCGFADLMGYIPVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
	151116176 Interest Voca Vocandario Valle Both I Aldrich Gest Sif Linding
SEQ ID NO:         ISOLATE           183         DK11           184         SW3           181         T8           182         US1           185         DK8	184 CCTVPVSA 184 CFTVPVSA 184 CFTVPVSA 184 CATVPVSA 184 CATVPVSA 184 CCTVPVSA
181-185 consensus	C-TVPVSA

#### FIGURE 7F

SEO ID NO: ISOLA'	
183 DK:	
184 SI	12
181	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
182 US	T MSINPAPUKAIAKNINKKPUDVKPPGGGOIVGGVYIIPRRGPRIGVRATPKTCEPCAPPCP
185 DI	ASTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVPATPKecependddad
186 St	1 MSTNPRPORKTRRNINRRPODVKFPGGGOIVGGVVI.I.pppGppiGVpATpkTcppcAppcp
178 US:	.v I MSTNPKPOKKTKKNTNKKPODVKFPGGGOIVGGVYLLPRRGPRICVRATDKTCFDCODDCD
180	.4 IMST1PRPORKTRRNTNRRPODVKFPGGGOIVGGVVLLPRRGPRIGVPATPKTGEDGODDCD
	.9 I MSTNPKPORKT1RNTNRRPODVKFPGGGOIVGGVYLLPRRGPRIGVR+TPKTGFRGADDGD
177	1 MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR
177-186 consensu	B MSTnPKPQRKTkRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSERSQPRGR
	-
SEO ID NO: ISOLAT	E
183 DK1	
184 SV	62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV
181	8 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGrV
182 US	1 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
185 DF	8 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
186 S8	3 04 KUPI PRUKKETURSWGI PGY PWPLYGNEGI GWAGWI.I.GDDGGDDGWGDTDDDULGDNT CVT
178 US1	V 02 KOPIPKDRKDIGKSWGKPGYPWPLYGNEGLGWAGWIJSPPGSPDSWGPTDDDUDSPROGEN
	4 04 KUPIPADAKSIGASWGKPGIPWPLYGNKGIAWAGWLLSDPGSDDSWGDandDDDDCDARACES
	5 62 KQPIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPendDubschmigyn
177	4 62 ROPIPKDRRSTGKSWGKPGYPWPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRHRSRNVGKV
177-186 consensu	
z,, zoo consense	E RQPIPKDRRBTGKBWGkPGYPWPLYGNEG-GWAGWLLSPRGSrPBWGPtDPRHrSRNlGkV
SEO ID NO: ISOLAT	
183 DK1	
184 SW	> 123 1D111CGFADLMGY1PVVGAPVGGVARALAHGVRVLEDGTNVATGNT.DGCGEGTETT.ATT.G
181	• 123 IDTITUGEADLMGYIPVVGAPVGGVARALAHGVRVT.RDGTNVATGNT.DGCGEGTETT.NTT.G
182	123 IDTITUGFADLMGYIPVVGAPVGGVARALAHGVRVT.RDGTNVATGNT.DGCGEGTETT NIT C
185 DK	• 143 IDIIICGFADLMGIIPVVGAPVGGVARALAHGVRVI.EDGINVATCNI.DCCCRCTRIIAIIC
186 S8	3 101UTUGFADLMGYIPVVGAPVGGVARATAHGVDVT.EDGTNVATGNT.DGCCDCTETTATTC
178 US1	V 123 IDIDICGEADLMGYIPVVGAPLGGVARALAHGVRVLEDGVNVATGNT DGCGEGTETT ATT C
180 T 179 T	2 123 IDILICGFADLMGYIPVVGAPLGGVARALAHGVRVT.RDGVNVATGNT.DGCCRCTRTT.RTTC
177 T	J 123 IDTLTUGFADLMGYIPVVGAPLGGVARALAHGVRVT.EDGVNVATGNT.DGCGEGTET.T.NT.C.
1//	123 IDTLTCsladlmgyvpvvggplggvaralahgvrvledgvnyatgnlpgcsfsifllalls
177-186 consensu	s IDT-TCgfADLMGYiPVVGaPvGGVARALAHGVRVLEDGiNYATGNLPGCSFSIFLLALLS
•	
SEO ID NO: ISOLAT	R
SEO ID NO: ISOLAT	
184 SW	
181 T	
182 US	
185 DK	
186 S8	
178 US1	
180 T	
179 T	
177 Ť	
177 196	
177-186 consensu	S CityPySA

#### FIGURE 7G

SEO ID NO:         ISOLATE           189         \$2           187         HK10           190         DK12           188         \$52	1 MSTLPKPORKTKRNTIRRPODIKFPGGGOIVGGVYVLPRRGPRLGVRATRKTSERSOPRGR 1 MSTLPKPORKTKRNTIRRPODVKFPGGGOIVGGVYVLPRRGPRLGVRATRKTSERSOPRGR 1 MSTLPKPORKTKRNTIRRPODVKFPGGGOIVGGVYVLPRRGPRLGVRATRKTSERSOPRGR 1 MSTLPKPORKTKRNTIRRPODVKFPGGGOIVGGVYVLPRRGPRLGVRATRKTSERSOPRGR
187-190 consensus	MSTLPKPQRKTKRNT1RRPQDvKFPGGGQ1VGGVYVLPRRGPRLGVRATRKTSERSQPRGR
SEQ ID NO:         ISOLATE           189         \$2           187         HK10           190         DK12           188         \$52           187-190         consensus	62 ROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV 62 ROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV 62 ROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV 62 ROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV ROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
SEO ID NO:         ISOLATE           189         \$2           187         HK10           190         DK12           188         \$52           187-190         Consensus	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS 123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS 124 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
SEO ID NO:         ISOLATE           189         S2           187         HK10           190         DK12           188         S52           187-190         consensus	184 CLIHPAAS 184 CLIHPAAS 184 CLIHPAAS 184 CLVHPAAS CLiHPAAS

#### FIGURE 7H

191-197 consensus	CLTvPaSA
	184 CLTVPASA
191 Z4 197 DK13	184 CLTVPASA
196 27	184 CLTVPASA
192 Z8 195 Z6	184 CLTVPASA 184 CLTVPtSA
193 Z1 192 Z8	184 CLTTPASA
194 25	184 CLTTPASA
SEO ID NO: ISOLATE	
191-197 consensus	IDTLTCGFADLMGYIP1VGAPVGGVARALAHGVRavEDGiNYATGNLPGCSFSIFLLAL1S
197 DK13	123 IDTLTCGFADLMGYIPvVGAPVGGVARALAHGVR11EDGvNYATGNLPGCSFSIFLLALLS
191 Z4	123 IDTLTCGFADLMGYIPi VGAPVGGVARALAHGVRAVEDGINVATGNI DGCESETEL ALLIS
195 Z6 196 Z7	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINVATGNI.DGCGEGIEII.NII.G
192 Z8	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGTNVATGNT.DGCGEGTETT.NTTG
193 21	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVPAVEDGINVATGNI.DGCGEGIELI ALI G
SEQ ID NO: ISOLATE	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRA1EDGINYATGNLPGCSFSIFLLALfS
191-197 consensus	RQPIPkARrsEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGpNDPRRRSRNLGKV
197 DK13	62 ROPIPKAROLEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRSRNLGKV
191 74	62 ROPIPKARODEGRSWAOPGYPWPLYGNEGCGWAGWILSPRGSRPSWGDNDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
195 196 27	62 ROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV 62 ROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
192 Z8 195 Z6	62 KQPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGDNDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
193 Z1	62 ROP1PKARRSEGRSWAOPGYPWPLYGNEGCGWAGWIJSPRGSRPSWGDNIDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
SEO ID NO: ISOLATE	62 ROPIPGARRSEGRSWAOPGYPWPLYGNEGCGWAGWLLSPRGSRPSWGGNDPRRRSRNLGKV
191-197 consensus	MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRatRKTSERSQPRGR
197 DK13	1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
191 Z4	1 MSTNPKPORKTKRNTNRRPMDVKFPGGGOTVGGVVI.I.DDDGDDI.GVDATDVTCEDCODDGD
196 27	1 MSTNPKPORKTKRNTNRRPMDVKFPGGGÖIVGGVYLLPRRGPRLGVRATRKTSERSÖPRGR 1 MSTNPKPORKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRLTRKTSERSÖPRGR
192 Z8 195 Z6	1 MSTNPKPORKTKRNTNRRPMDVKFPGGGOIVGGVYLLPRRGPRIGVRATDKTGEDGÖDDGD
193 Z1	I MAINPAPURAIARNINKRPMUVKFPGGGOIVGGVYII.PRRGPRIGVRAADKTCEDCODDCD
SEO ID NO: ISOLATE 194 Z5	1 MSTNPKPORKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRALRKTSERSQPRGR
CEC ID NO. ISOLATE	

## FIGURE 71

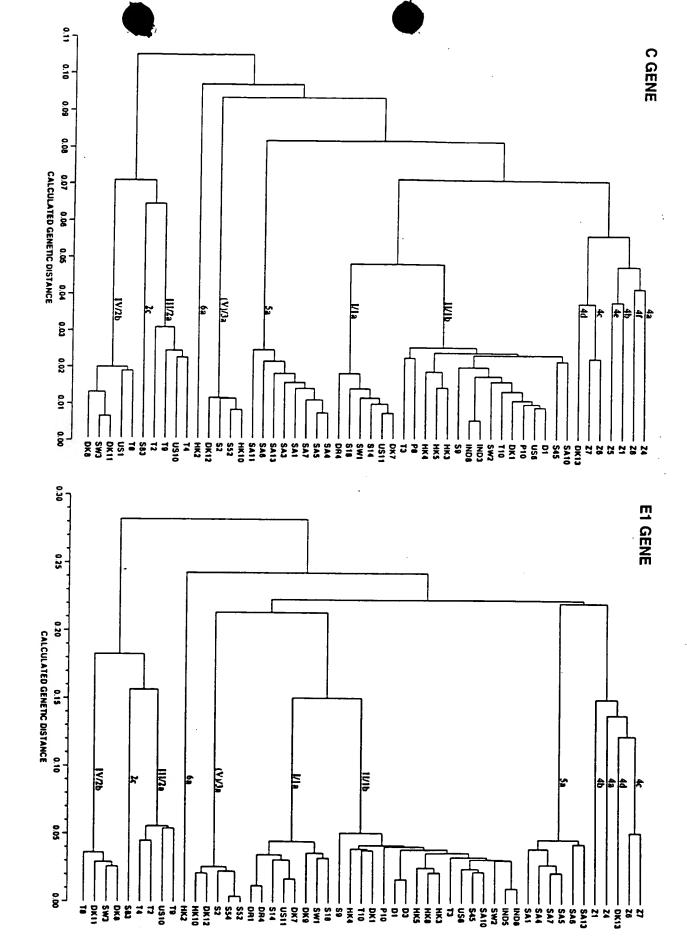
SEO ID NO:         ISOLATE           205         SA11           202         SA3           198         SA4           199         SA5           200         SA7           203         SA13           201         SA1           204         SA6           198-205         Consensus	1 MSTNPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTNPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTNPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTNPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTNPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTNPKPORKTKRNTNRRPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTNPKPORKTKRNTN1RPODVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSOPRGR 1 MSTNPKPORKTGRNTN*RPODVKFPGGGQIVGGVYLLPRRGPRMGVRATRKTSERSOPRGR MSTNPKPORKTKRNTN*RPODVKFPGGGQIVGGVYLLPRRGPRMGVRATRKTSERSOPRGR
SEO ID NO:         ISOLATE           205         SA11           202         SA3           198         SA4           199         SA5           200         SA7           203         SA13           201         SA1           204         SA6           198-205         Consensus	62 ROPIPKAROPTGRSWGOPGYPWPfYANEGLGWAGWLLSPRGSRPNWGPNDPRR'SRNLGKV 62 ROPIPKAROPTGRSWGOPGYPWPLYANEGLEWAGWLLSPRGSRPSWGPNDPRRKSRNLGKV 62 ROPIPKAROPTGRSWGOPGYPWPLYANEGLGWAGWLLSPRGSRPNWGPNDPRRKSRNLGKV 62 ROPIPKAROPTGRSWGOPGYPWPLYANEGLGWAGWLLSPRGSRPNWGPNDPRRKSRNLGKV 62 ROPIPKAROPTGRSWGOPGYPWPLYANEGLGWAGWLLSPRGSRPNWGPNDPRRKSRNLGKV 62 ROPIPKAROPTGRSWGOPGYPWPLYANEGLGWAGWLLSPRGSRPNWGPNDPRRKSRNLGKV 62 ROPIPKAROPTGRSWGOPGYPWPLYANEGLGWAGWLLSPRGSRPNWGPNDPRRKSRNLGKV 62 ROPIPKAROPTGRSWGOPGYPWPLYANEGLGWAGWLLSPRGSRPNWGPNDPRRKSRNLGKV 63 ROPIPKAROPTGRSWGOPGYPWPLYANEGLGWAGWLLSPRGSRPNWGPNDPRRKSRNLGKV
SEO ID NO:         ISOLATE           205         SA11           202         SA3           198         SA4           199         SA5           200         SA7           203         SA13           201         SA1           204         SA6           198-205         consensus	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRALEDGVNYATGNLPGCSFSIFILALLS 123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFILALLS 124 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFILALLS 125 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFILALLS 126 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFILALLS 127 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFILALLS 128 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFILALLS 129 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFVLALLS 120 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFVLALLS 121 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFILALLS
SEO ID NO:         ISOLATE           205         SA11           202         SA3           198         SA4           199         SA5           200         SA7           203         SA13           201         SA1           204         SA6           198-205         Consensus	184 CLTVPATA 184 CLTVPASA 184 CLTVPASA 184 CLTVPASA 184 CLTVPASA 184 CLTVPESA 184 CLTVPESA 184 CLipasa 184 CLipasa CLtvPasa

# PIGURE 7J

_			•
1 MSTNPKPQRKTKRNTNrRPqDvKFPGGGQIVGGVYlLPRRGPRlGVRatRKtSERSQPRGRRQPIPkaRrpeGraWaqPGyPWPlYgnBGcgWAGW	MSTNPKPORKTKRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRALRKTSERSOPRGRROPIPKARFPEGRAWAOPGYPWPLYGNEG-GWAGW MSTNPKPORTFRNTNRRPODVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGRROPIPKARRSEGRSWAOPGYPWPLYGNEGIGWAGW MSTLPKPORTTKRNTIRRPODVKFPGGGOIVGGVYVLPRRGPRLGVRATRKTSERSOPRGRROPIPKARRSEGRSWAOPGYPWPLYGNEGCGWAGW MSTNPKPORTKRNTNRRPMDVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGRROPIPKARFEGRSWAOPGYPWPLYGNEGCGWAGW MSTNPKPORKTKRNTNRRPMDVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGRROPIPKARQPCGRSWGOPGYPWPLYGNEGCGWAGW MSTNPKPORKTKRNTNRRPTDVKFPGGGOIVGGVYLLPRRGPRLGVRATRKTSERSOPRGRROPIPKARQPGSRHWAOPGYPWPLYGNEGCGWAGW	97 LLSPrGSrPaWGptDPRrrSRN1GkVIDT11CgfADLMGYiPlvGaP1GGvArALAHGVRv1EDGvNyATGN1PGCaFSIF1LAL1SC1tvPasa	LLSPrGSRPBWGPtDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGaPLGGBARALAHGVRVIEDGVNYATGNIPGCBFSIFLLALLSCLTTIPASA LLSPRGSrPBWGPtDPRHrSRNIGKVIDT1TCGfADLMGYIPVVGaPvGGVARALAHGVRVLEDGINYATGNIPGCSFSIFLLALLSCLTvPvSA LLSPRGSRPSWGPNDPRRRSRNLGKVIDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNIPGCSFSIFLLALFSCLIHPAAS LLSPRGSRPSWGPNDPRRRSRNLGKVIDTLTCGFADLMGYIPIVGAPVGGVARALAHGVRAVEDGINYATGNIPGCSFSIFLLALISCLTvPaSA LLSPRGSRPNWGPNDPRRKSRNLGKVIDTLTCGFADLMGYIPIVGGPVGGVARALAHGVRAVEDGINYATGNIPGCSFSIFILALLSCLTVPASA LLSPRGSRPHWGPNDPRRKSRNLGKVIDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNIPGCSFSIFILALLSCLTVPASA LLSPRGSRPHWGPNDPRRKSRNLGKVIDTLTCGFADLMGYIPVVGAPLGGVARALAHGVRAIEDGINYATGNIPGCSFSIFILALLSCLTYPASA
, De			
Genotype cons.	type type type type type	Genotype cons.	type 2 type 3 type 4 type 5 type 5
SEQ ID NO: 155-206	155-176 177-186 187-190 191-197 198-205	SEO ID NO: 155-206	155-176 177-186 187-190 191-197 198-205

# FIGURE 7X

06	  EGCGWAGW	22222222222222	190	LISCITYP858	
8.	MST nPKPQRKT KRNT NFRP GDVK FPGGGG I VGGVY I L PRIGPRI GVR B t ÅK t SERSQPRGRRQP I PKBR I PEGFSWAGP GYPUP I YGNEGCANAGW	M. K.K. NR O-V    N. K.K. NR O	180	IFILA 1SC	R. R. S. PT . RR . L . K L . GF L . A . L . A . R
€0	eGrsWaqP	CERT - A0-	170	NIPGCSFS	
6	 aPIPkaRrp	######################################	<b>9</b> 4	DGVNYATG	
9	RSOPRGRR			LAHGVRVLE	
\$0	VRBERKESE	A	150	PIGGVAFA	
0,	Prrgprig		140	HGY IP LYG	
30	olvecvill		130	TITC9fADI	
oz ⁻	dovKFPGG	>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>>	120	SRWIČKVID	25 65 65 65 65 65 65 65 65 65 65 65 65 65
ē	<b>IKRNT</b> nrRP	**************************************	011	, Kpt0PRrr!	
5_	TrPKPGRK		8-	LLSPrGSrPaugatoprersrnigkvidtitgfadingyipiygapiggvaralangvrviedgvnyatgnipggsfsifila	R S S P T S S P T S S P T S S P T S S P T S S P T S S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S P T S
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	Genotype	1/19 11/16 11/28 20/1/28 46 46 46 46 46 46 46 46 68		Genotype	1/10 11/16 11/26 20 (V)/38 46 46 46 46 46 46
	EQ 10 NO:	55-160 77-180 77-180 88-190 93-205 98-205		EQ ID NO:	55-160 61-176 77-180 81-185 87-190 93-205



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